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ilarity Conserva	UGLT 1 08-525-596B-6 equence 6, Application US/0 equence 6, Application US/0 etcant No. 5827733 BENERAL INCORMATION: APPLICANT: Lee, Se-Jin TITLE OF INVENTION: GROWN NUMBER OF SEQUENCES: 32 CORRESSONDENCE ADDRESS: ADDRESSEE: Fish & Rich STATE: CA COUNTRY: US ZIP: 92037 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatib OPERATION SYSTEM: Wind SOFTWARE: FastSEQ for CURRENT APPLICATION DATA: APPLICATION NUMBER: US FILING DATE: 19-SEP- CLASSIFICATION LATA: APPLICATION NUMBER: US FILING DATE: 08-JUL-19 ATTORNEY/AGENT INFORMATIC NAME: Wetherell, Jr. REGISTRATION NUMBER: 3 REFERENCE/DOCKET NUMBER TELECOMMUTICATION INFORMATIC NAME: Wetherell, Jr. REGISTRATION NUMBER: 3 REFERENCE/DOCKET NUMBER TELECOMMUTICATION SICH TELEPHONE: 619-678-507 TELEPHONE: 619-678-507 TELEPTON FOR SEQ ID NO. SEQUENCE CHARACTERISTICS: LENGTH: 126 amino acid TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal 08-525-596B-6		7775.0 75.0 75.0 75.0 75.0 75.0 75.0 75.
80.4 80.7 tive	1 1 25-596B-6 nce 6, Application US/0852556 nce 6, Application US/0852556 t No. 5827733 RAL INFORMATION: PLICANT: Huyth, Thanh PLICANT: Lee, Se-Jin PLICANT: Lee, Se-Jin MBER OF SEQUENCES: 32 MBER OF SEASTANT ON SQUARE COUNTRY: US ZIP: 92037 ZIP: 92037 ZIP: 92037 MBUTTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OCCOMPUTER: IBM Compatible OCCOMPUTER: LEM COMPATIBLE MEDIUM TYPE: DIskette COMPUTER: J9-SEP-1995 SOFTWARE: FASTSEQ for Windows MAPPLICATION NUMBER: US/08/525 FILING DATE: 19-SEP-1995 CLASSIFICATION NUMBER: PCT/US94/ TILING DATE: 08-UUI-1994 TORNET/AGENT INFORMATION: MARE: Wetherell, Jr., Ph.D., J REGISTRATION NUMBER: 31,678 MAPPLICATION NUMBER: 0778 TELEPHONE: 619-678-5070 TELEPHONE: 619-678-5070 TELEPHONE: 619-678-5070 TELEPAX: 619-678-5070 TELEPHONE: 619-678-5070 TELEPAX: 619-678-5070 TELEPHONE: 619		375 4 375 4 375 4 375 4 374 4 1126 4 1126 1 126 2 362 1 362 1
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                                                                 Sequence 6, Application US/09378238 Patent No. 6465239 GENERAL INFORMATION:
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          APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO:
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APPLICANT: Huynh, Thanh
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/52:
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Haile, Ph.D, Lisa A. REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: FRAGMENT TYPE:
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RESULT 4
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EARLIER FILING DATE: 1994-03-18
EARLIER APPLICATION NUMBER: 08/033,923
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SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 1999-08-19
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ORGANISM: Mus musculus
                                           INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 4225 EX CITY: La Jolla STATE: CA
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                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 30-No. 64685: CLASSIFICATION: <Unknown>
                                                                                                                                                     NAME: Lisa A. Haile, Ph.D. REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: Windows95
                                                                                       TELEPHONE: 619/678-50
TELEFAX: 619/678-5099
                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US94/03019 FILING DATE: 18-March-1994
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/795,071 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/451,501 FILING DATE: 30-No. 6468535-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                       ENGTH:
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H: 126 amino acids
amino acid
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80.7%;
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Pred. No. 6.7e-52;
1; Mismatches 11
                                                                                                                                                          07265/105001
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US-09-378-238-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Rattus norvegicus US-09-378-238-21
                             GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES
TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/09378238 Patent No. 6465239
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Best Local
                                                                                                                                         Sequence 19, Application US/09378238 Patent No. 6465239
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1997-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 08/
EARLIER FILING DATE: 1993-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1994-03-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lee, Se-Jin APPLICANT: McPherron, Alexandra C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: JHU1120-9
CURRENT APPLICATION NUMBER: US/09/378,238
                  FILE REFERENCE: JHU1120-9
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CURRENT APPLICATION NUMBER: US/09/378,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                 18
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                                                                                                                                                                                                                                                                                                                                        DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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; LENGTH: 225
; TYPE: PRT
; ORGANISM: Gallus g
US-09-378-238-19
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US-08-525-596B-14
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US-08-525-596B-14
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: FRASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
FILING DATE: 19-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US94/07762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                          APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07265/07500
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
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EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 41
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EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
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EARLIER APPLICATION NUMBER: 08/795,071
                                                                                                                                       TELEFAX: 619-678-5099 INFORMATION FOR SEQ ID NO:
                  MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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                                                          TOPOLOGY:
                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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o. 5827733
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92; Conserv
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                                                                                                 375 amino acids
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Pred. No. 1.4e-51;
' Mismatches 11;
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US-08-765-875-5
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                                                                                                                                                                                                                                                                                                                TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PD:
REFERENCE/DOCKET NUMBER: PD:
TELEPHONE: 619/455-5100
                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acid
                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN PH.D., LISA A.
REGISTRATION NUMBER: P-38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LEE, SE-JIN
APPLICANT: MCPHERRON, ALEXANDRA C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
                                                                                                                                                                                                         IMMEDIATE SOURCE:
   267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322
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                                                                                                                                                                                        CLONE:
                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PKVSASHL-;----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                               Local
                                                                                                                                         LOCATION:
                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 08-JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: LOS ANGELES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFUNFTVSFWLRV 60
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DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF----
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                                                                             Similarity
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                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                          GDF-8
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                                                                                                                                                                                                                                                                                  375 amino acids
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1880 CENTURY PARK EAST, FIFTH FLOOR
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                                                               Conservative
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                                                        Score 501; DB z; L
Pred. No. 2.5e-51;
Pred. No. 2.11;
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Pred. No. 2.5e-51;
1; Mismatches 11
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                                                                                         Length 375;
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-VFLQKY 321
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US-09-177-860A-14
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US-08-795-671-5
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                                                                                                     Sequence 14, Application US/09177860A Patent No. 6096506
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Patent No. 6008434
GENERAL INFORMATION:
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                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
TELECOMMUNICATION INFORMATION:
                APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVERTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                322 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/795,671 FILING DATE: February 6, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
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                                                                                                                                                                                                                                                                                                          1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
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92; Conserv
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E: Gray Cary Ware & Freidenrich LLP 4365 Executive Drive, Suite 1600

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                                                                           ; TYPE: PRT; ORGANISM: Homo sapiens US-09-252-1498-29
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                                                                                                                         PRIOR APPLICATION NUMBER: 60/075,213
PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 29
LENGTH: 375
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Barker, Christopher A.
APPLICANT: Morsey, Wohamad
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
TITLE OF INVENTION: VERTEBRATE SUBJECTS
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/09252149B
Patent No. 6369201
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   Matches
                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                FILE REFERENCE: 9001-0042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92121
COMPUTER READABLE FORM:
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LENGTH: 375 amino acids
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APPLICATION NUMBER: US
FILING DATE: 23-OCT-19
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STREET: 4365 Exec
CITY: San Diego
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SOFTWARE: FastSEQ for Windows Version 2.0
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REFERENCE/DOCKET NUMBER: 07265/075003
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92; Conservative
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   Conservative
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80.7%;
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Score 501; DB 4; Length 375; Pred. No. 2.5e-51; 1; Mismatches 11; Indels

    Mismatches

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В
                                                                                                                                                    ; ORGANISM: Gallus gallus US-09-252-149B-34
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PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 32
LENGTH: 375
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APPLICANT: Barker, Christopher A.
APPLICANT: Morsey, Mohamad
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
TITLE OF INVENTION: VERTEBRATE SUBJECTS
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Barker, Christopher A.
APPLICANT: Morsey, Mohamad
                                                                                                                                                                                                                               SEQ ID NO 34
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Best Local :
                                                                           Matches
                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,149B CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: 60/075,213 PRIOR FILING DATE: 1998-02-19 NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Morsey, Mohamad TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN TITLE OF INVENTION: VERVEBRATE SUBJECTS FILE REFERENCE: 9001-0042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,149B CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                         TYPE: PRT
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                                                                  Score 501; Db 4; Pred. No. 2.5e-51; """ amatches 11;
                                                                                                              DB 4; Length 375;
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US-09-378-238-14
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US-09-252-149B-35
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EARLIER APPLICATION NUMBER: 08/795,071
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: 05/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER FILING DATE: 1994-03-18
EARLIER FILING DATE: 1994-03-18
EARLIER FILING DATE: 1994-03-19
EARLIER FILING DATE: 1993-03-19
RUMBER OF SEO ID NOS: 41
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LENGTH: 375
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APPLICANT: Morsey, Mohamad
TITLE OF INVENTION: IMMUNICOSICAL METHODS TO MODULAR MYOSTATIN IN
TITLE OF INVENTICN: VERTEBRATE SUBJECTS
FILE REFERENCE: 9001-0042
CURRENT APPLICATION NUMBER: US/09/252,149B
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION UMMBER: 60/075,213
PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 39
SOFTMARE: Patentin Ver. 2.0
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APPLICANT: McPhetron, Alexandra C.
APPLICANT: McPhetron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPETIDES FROM AQUATIC SPECIES AND NON-HUMAN
TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
FILE REFERENCE: JULI120-9
FI
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80.7%; Pred. No. 2.5e-51;
tive 1; Mismatches 11; Indels
        Score 501; DB 4;
Pred. No. 2.5e-51;
1; Mismatches 11;
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Perfect score:
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   Published_Applications_AA:*

1: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

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US-09-859-211-33
US-09-859-211-35
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416.242 Million cell updates/sec
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US-08-981-490B-4	US-09-813-398-22	US-09-813-398-20	US-09-880-708-24	US-09-859-211-46	US-10-115-406-20	US-09-813-459-20	US-09-205-658-317	US-09-859-211-8	US-09-841-730-27	US-09-841-730-29	US-09-813-398-33	US-09-859-894A-2	US-09-454-540-6	US-09-454-540-2	US-09-841-730-25	US-09-859-894A-4	US-09-454-540-4	US-09-841-730-20	US-09-859-211-21	US-09-841-730-12	US-09-754-826-2	US-09-859-211-19	US-09-841-730-10	US-09-859-894A-5	US-09-859-211-31
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ALIGNMENTS

Searched:

Run on:

NURLE FASLES SOFTWARE: FASLES SOFTWARE: FASLES FOR THE 126 CURRENT APPLICATION NUMBER: US/09/859,211 CURRENT FILING DATE: 2001-05-15 PRIOR APPLICATION NUMBER: 09/019,070 PRIOR FILING DATE: 1998-02-05 PRIOR APPLICATION NUMBER: 08/862,445 PRIOR APPLICATION NUMBER: 08/847,910 PRIOR FILING DATE: 1997-05-23 PRIOR PPRIOR DATE: 1997-04-28 PRIOR APPLICATION NUMBER: 08/795,071 PRIOR APPLICATION NUMBER: 08/795,071 PRIOR APPLICATION NUMBER: 08/795,071 PRIOR APPLICATION NUMBER: 08/795,071 PRIOR FILING DATE: 1997-02-05 GENERAL INFORMATION: APPLICANT: Lee, Se-Jin APPLICANT: McPherron, Alexan TITLE OF INVENTION: GROWTH D. FILE REFERENCE: 07265/144001 Sequence 6, Application US/09859211 Patent No. US20020157125A1 PRIOR APPLICATION NUMBER: PCT/US94/03019 PRIOR FILING DATE: 1994-03-18 PRIOR APPLICATION NUMBER: 08/033,923 PRIOR FILING DATE: 1993-03-19 PRIOR APPLICATION NUMBER: 08/525,596 PRIOR FILING DATE: 1995-10-26 LENGTH: 126 TYPE: PRT ORGANISM: Mus musculus PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109 l Similarity 80.7 92; Conservative FastSEQ NOS: 51 Q for Windows Version 4.0 80.4%; Alexandra DIFFERENTIATION FACTOR-8 Score 501; DB 9; Pred. No. 1.7e-43; 1; Mismatches 11 <u>ი</u> Length 126; 10;

Gaps

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Result No.

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US-09-859-211-33; Sequence 33, Application US/09859211; Patent No. US20020157125A1
                                                    CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
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PRIOR APPLICATION NUMBER: 08/862,445
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PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/09859211 Patent No. US20020157125A1
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                                                                                                                                                                                                                                                                                 APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
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CURRENT FILING DATE: 2001-05-15
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PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
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Local Similarity 80.7%;
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                                        FILING DATE: 1997-02-05
APPLICATION NUMBER: 08/525,596
FILING DATE: 1995-10-26
APPLICATION NUMBER: PCT/US94/03019 FILING DATE: 1994-03-18
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    Mismatches

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RESULT 5
US-09-841-730-2
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; Patent No. US20020157126A1
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GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND M
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 374
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
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Best Local Similarity
Matches 92; Conserv
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APPLICANT: Lee, Se-
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TITLE OF INVENTION: GROWTH DIFFERNTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND PETLE REFERENCE: JHU1470-2
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PRIOR TILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
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  AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING
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80.7%;
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Pred. No. 4.9e-43;
1; Mismatches 11
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PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR EILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR PILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
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Best Local
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PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
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APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
FILE REFERENCE: JHU1470-2
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER
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TYPE: PRT
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322 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
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                                                                                                   267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY 321
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                                                                                                                                                                                                                          80.4%; Score 501; DB 9; Length 375; 80.7%; Pred. No. 4.9e-43;

    Mismatches

    Mismatches

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; ORGANISM: Homo sapiens US-09-859-211-14
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                                              SEQ ID NO 14
LENGTH: 375
TYPE: PRT
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TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
FILE REFERENCE: JHU1470-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-08-01
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PRIOR FILING DATE: 2000-01-31
                                                                                                                                                         PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
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                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1997-04-28
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PRIOR FILING DATE: 1997-05-23
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                                                                                                                                            NUMBER OF SEQ ID NOS: 51
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92; Conserv
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UMBER: 08/862,445
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; ORGANISM: Gallus gallus US-09-859-211-23
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US-09-859-211-23
                                                                                                                                                                                                   GENERAL INFORMATION:
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                APPLICANT: Lee, Se-Jin
APPLICANT: McPherton, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFÉRENCE: 07265/144001
CURRENT ÁPPLICATION NUMBER: US/09/859,211
CURRENT ÁPPLICATION NUMBER: 09/019,070
PRIOR APPLICATION NUMBER: 09/019,070
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APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
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PRIOR FILLING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILLING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/03,923
PRIOR FILLING DATE: 1993-03-19
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PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
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PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
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PRIOR FILING DATE: 1998-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
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NUMBER OF SEQ ID NOS: 51
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    Mismatches

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PRIOR APPLICATION NUMBER: 08/795,071
PRIOR PILING DATE: 1997-02-05
PRIOR PELLING DATE: 1997-02-05
PRIOR PELLING DATE: 1995-10-26
PRIOR PELLING DATE: 1995-10-26
PRIOR PELLING DATE: 1994-03-18
PRIOR PELLING DATE: 1994-03-18
PRIOR PELLING DATE: 1994-03-19
PRIOR PELLING DATE: 1993-03-19
PRIOR PELLING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SECTIMARE: FASTSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 27
LENGTH: 375
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; SEQ ID NO 29
; LENGTH: 375
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                                                                                       Matches 92; Conservative
                                                                                                                                     Query Match
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CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
CURRENT FILING DATE: 2001-05-15
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PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR FILING DATE: 1997-02-05
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PRIOR FILING DATE: 1994-03-18
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APPLICANT: McPherron, Alexandra C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/019,070
                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Porcine
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80.7%;
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    Mismatches

    Mismatches

                                                                                                              Score 501; DB 9; Length 375; Pred. No. 4.9e-43;
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61 PKVSASHL----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109

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US-09-454-540-5
           RESULT 13
US-09-841-730-4
Sequence 4, Application US/09841730
; Patent No. US20020157126A1
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Patent No. US20010053358A1
GENERAL INFORMATION:
APPLICANT: Se-Jin Lee and Alexar
GENERAL
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                      Query Match
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APPLICATION NUMBER: 08/795,671
FILING DATE: February 6, 1997
CLASSIFICATION:
ATTORNEY,AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 07265/106001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Se-Jin Lee and Alexandra McPherron
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: 619/678-5070
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CLONE: GDF-8
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                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                       Local Similarity
nes 92; Conserv
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                                                                                                                                                                        DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY
                                                                                                           INFORMATION:
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4225 Executive Square, Suite 1400
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Pred. No. 4.9e-43;
1; Mismatches 11
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US-09-841-730-6
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Best Local Similarity
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PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/1:
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
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CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/485,046
PRIOR EILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR EILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR EILING DATE: 1997-08-01
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TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS, TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND FILE REFERENCE: JHU1470-2
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-07-27
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APPLICANT: McPherron, Alexandra C.
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61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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Pred. No. 4.9e-43;
1; Mismatches 11
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                                                                                                                 Score 501; DB 9;
Pred. No. 4.9e-43;
1; Mismatches 11
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323 PHTHLYHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 376

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RESULT 15

US-09-859-211-12

US-09-859-211-12

Sequence 12, Application US/09859211

Patent No. US20020157125A1

GENERAL INFORMATION.

APPLICANT: Lee, Sey-Jin

APPLICANT: Metherion, Alexandra C.

TITLE OF INVERTION. GROWTH DIFFERENTIATION FACTOR-8

FILE REFERENCE: 07565/144001

CURRENT FILING DATE: 1986-02-05

PRIOR PAPLICATION NUMBER: 08/09/859/211

CURRENT FILING DATE: 1997-02-05

PRIOR PAPLICATION NUMBER: 08/862,445

PRIOR PAPLICATION NUMBER: 08/817/910

PRIOR PAPLICATION NUMBER: 08/817/910

PRIOR PAPLICATION NUMBER: 08/817/910

PRIOR PAPLICATION NUMBER: 08/795,071

PRIOR PRIOR DATE: 1997-02-05

PRIOR PRILING DATE: 1997-02-05

PRIOR PRILING DATE: 1993-03-18

PRIOR PRILING DATE: 1993-03-18

PRIOR PRILING DATE: 1993-03-19

PRIOR APPLICATION NUMBER: 08/03/923

PRIOR PRILING DATE: 1993-03-19

PRIOR PRILING DATE: 1993-03-18

PRIOR PRILING DATE: 1993-03-18

PRIOR PRILING DATE: 1993-03-19

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Maximum Match 100%
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Maximum DB
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA2900.DAT: *
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Human TGFbeta prot
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	Meleagris gallopav	Porcine promyostat	Chicken promyostat	Human promyostatin	Pig growth differe	Chicken growth dif	Human growth diffe	Human GDF-8 #2. H	Human growth diffe	Human growth diffe	Human GDF-8. Homo	Human myostatin.	Turkey GDF-8 prote	٠	8 prote	Amino acid sequenc							Amino acid sequenc		eque	Human growth diffe	an growth d	ω,	cken growth	ff	n promyost	Turkey growth diff	n GDF-8.	Growth differentia

ALIGNMENTS

AAB20149 standard; Protein; 109

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ARESULT 1
AAB20149
ID AAB2
XX AAB2
XX AAB2
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DT 30-A
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COLUMN
XX Grow
XX Grow
XX Chim
OS Chim
OS Chim
OS Chim
FT Regi
FT Regi Growth differentiation factor 8; T-cell epitope; down-regulation; cardiant; human; mutant; mutein. Chimeric - Homo sapiens. Chimeric - Clostridium tetani Misc-difference 90..91 /note= Misc-difference Region Synthetic. Growth differentiation factor 8 AutoVac construct GDF-8 P30-2. 30-APR-2001 (first entry) Region Region 73 /note= "70..109 /note= 49..69 /note= "identical to residues 267-314
 GDF-8" /note= Location/Qualifiers "tetanus toxoid P2 epitope" "optionally replaced by Glu-Gly" "Cys-73 may be substituted by Ser disulfide bond formation" "identical to residues 336-375 GDF-8" GDF-8; myostatin; tetanus toxin; vaccine; muscle; meat; cachexia; of human of to avoid human

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of AutoVac construct GDF-8 p30-2, comprising the 109 C-terminal amino acid residues of human growth differentiation factor 8 (GDF-8) in which residues 49-69 are replaced by the promiscuous tetanus toxin T-cell epitope p30 (see AAB20144). It is an object of the invention to produce a recombinant therapeutic vaccine that is capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. The vaccines (see AAB20145-53) are capable of breaking autotolerance against autologous GDF-8. They comprise
          Chimeric - Chimeric -
                                                                                                      Growth differentiation factor 8; T-cell epitope; down-regulation;
                                                                                                                                                                            Growth differentiation factor 8 AutoVac construct GDF-8
                                                                                                                                                                                                                                   30-APR-2001
                                                                                                                                                                                                                                                                                     AAB20152;
                                                                                                                                                                                                                                                                                                                                  AAB20152 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increasing the muscle mass of animals used in meat production by deregulating growth differentiation factor 8 (GDF-8) activity in the animal through induction of anti-GDF-8 antibody production -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 101-102; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halkier T, Mouritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEBI-) M & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-2000; 2000WO-DK00413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200105820-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PKVSASHLEAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKVSASHLEAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-112680/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                              human; mutant; mutein
       Clostridium tetani
                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOTECH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99DK-0001014
99US-0145275
                                                                                                      down-regulation; vaccine; muscle; meat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 623; DB 22; 100.0%; Pred. No. 3.2e-60; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klysner
                                                                                                                                                                                                                                                                                                                                    254
                                                                                                                             GDF-8; myostatin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                           tetanus toxin;
                                                                                                                                                                               dimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
γΩ
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                                                                                              QΥ
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Query Match
Best Local
                                                                                                            Matches
                                                                                                                                                                                                                                                                            The present sequence is that of AutoVac construct GDF-8 dimer comprising 2 copies of the 109-amino acid C-terminal region of huma growth differentiation factor 8 (GDF-8, see AAF20141) covalently connected through the P2 and P30 T-cell epitopes (see AB20143-44) of tetanus toxin. It is an object of the invention to produce a recombinant therapeutic vaccine that is capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. The vaccines (see AB20145-53) are capable of breaking autotolerance against autologous GDF-8. They comprise
                                                                                                                                                                                              antibiotic feed-additives. Anti-GDF8 vaccines can be used to treat human diseases such as cancer cachexia where muscle atrophy is pronounced and for patients suffering from acute and chronic heart
                                                                                                                                                                                                                                          the protein. Nucleic acids encoding the GDF-8 variants can be used for genetic immunisation of the animals. Down-regulation of GDF-8 activity can increase muscle mass by up to at least 45% in cattle, pigs and poultry used for meat production, reducing the need for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Increasing the muscle mass of animals used in meat production by regulating growth differentiation factor 8 (GDF-8) activity in the animal through induction of anti-GDF-8 antibody production -
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 105-106; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-112680/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halkier T, Mouritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MEBI-) M & E BIOTECH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-2000; 2000WO-DK00413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200105820-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
    61
                             49
                                                        ب
VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCSQYIKANSKFIG 120
                                                  DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECE-------
                                                                                                                        Similarity
                                                                                                                                                                 254
                                                                                                         Conservative
                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "tetanus toxoid P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99DK-0001014
99US-0145275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "optionally 235..236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "109 C-terminal residues of human 90..91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "109 C-terminal residues of human 110...124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                      85.2%;
42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "optionally replaced by Glu-Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klysner
                                                                                                        Score 530.5; DB 2
Pred. No. 9.9e-50;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toxoid P2 epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replaced by Glu-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P30 epitope"
                                                                                                                                 DB 22;
                                                                                                         0;
                                                                                                         Indels
                                                                                                                                 Length
                                                                                                         145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDF-8"
                                                                                                                                   254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDF-8"
                                                                                                                                                                                                                                                                                                                                                                                                                                    of human
                                                                                                       Gaps
                          48
                                                                               48
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2;

Best Local Similarity

79.5%;

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RESULT 3
AAY 3 384 5
ID AAY 3 384 5
AC AAY 3
AC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    рь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                            GDF-8 has been shown to result in increased bone and muscle mass as ribs) when expressed in reduced amounts. GDF-8 minus transgeni animals and forms of animal feed that can inhibit/reduce producti GDF-8 are of commercial interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell differentiation; animal feed; muscle disorder; bone degeneration; nerve degeneration; GDF-8; development; transforming growth factor beta; TGF-beta.
   Sequence
                                                                                     as muscle wasting disease, neuro muscular disorder, muscle atrophy, osteoporosis, bone degenerative diseases, obesity or other adipocyte
                                                                                                                                            of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8 antisense molecule or dominant negative polypeptide could be used with foetal or adult muscle cells, bone cells or progenitor cells. These agents can be administered to a patient suffering from a disorder such
                                                                                                                                                                                                                                                                 GDF-8 expression may also have a role in the therapy of abnormal growth
                                                                                                                                                                                                                                                                                                                                                                                                             Differentiation Factor-8 (GDF-8). Skeletal muscle cDNA libraries from this species were screened with the murine GDF-8 probe, in order to isolate the GDF-8. The absolute conservation of the C-terminal region between species as evolutionary far apart as humans and chickens, baboons and turkeys, suggests that this region will be highly conserved in many other species as well.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Fig 14g; 138pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1998;
05-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9940181-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY33845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New differentiation factor useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYJO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ITELFNNFTVSFWLRVPKVSASHLEDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is the amino acid sequence of the Ovine Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-494289/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRYKANYCSGECEFVFLQKYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McPherron AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0124180
98US-0019070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US02511
                                                          and aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor; tissue growth; muscle growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovine Growth Differentiation Factor-8
                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375 AA
                                                          example.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGPCCTPTKMSPINMLYFNGKEQIIY
                                                                                                                                                                                                                                                                                                                                                         minus transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                  highly conserved
                                                                                                                                                                                                                                                                                                                              production of
                                                                                                                                                                                                                                                                                                                                                                                           (such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
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Query Match

80.98;

Score

504;

DB 20;

Length 375;

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RESULT 4
AAB20141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID
                                                                                                                                                        The present sequence comprises the 109 amino acid residue
C-terminal region of human growth differentiation factor 8
(GDF-8), i.e. residues 267-375 of the full-length protein (see
CG (GDF-8), i.e. residues 267-375 of the full-length protein (see
CC AAB20131). The homodimer of this region is thought to be the
CC invention to produce a recombinant therapeutic vaccine capable of
CC invention to produce a recombinant therapeutic vaccine capable of
CC effecting down-regulation of GDF-8 in order to increase the muscle
CC growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)
CC are provided that are capable of breaking autotolerance against
CC autologous GDF-8. These comprise the C-terminal portion of human
CC GDF-8 in which a portion of the native sequence is replaced by a
CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
CC p2 or p30. The high number (9) of Cys residues in the C-terminal
CC region limits the possible sites in which the T-cell epitope can be
CC positioned without major disturbance of the native 3-dimensional
CC structure of the protein Number (20) of Cys residues in the C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                         of GDF-8 cattle, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 93-94; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Increasing the muscle mass of animals used in meat production by deregulating growth differentiation factor 8 (GDF-8) activity in the animal through induction of anti-GDF-8 antibody production \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Growth differentiation factor 8; GDF-8; myostatin; down-regulation; vaccine; muscle; meat; cachexia; cardiant; human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-2001
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                                                                     of GDF-8 activity can increase muscle mass by up to at least 459 cattle, pigs and poultry used for meat production, reducing the for antibiotic feed-additives. Anti-GDF8 vaccines can be used t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
               pronounced
failure.
                                                   for antibiotic feed-additives. Anti-GDF8 vaccines can be used to treat human diseases such as cancer cachexia where muscle atrophy is
                                                                                                                            can be used for genetic immunisation of the animals.
                                                                                                                                              structure of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-112680/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-2000; 2000WO-DK00413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MEBI-) M & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PKVSASHL-------EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEENNETVSEWLRV
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                                 and for patients suffering from acute and chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99DK-0001014
99US-0145275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klysner S;
                                                                                                                                              Nucleic acids encoding the GDF-8 variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.2e-46; 2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor 8 C-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
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                                                                                                                              Down-regulation
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AAM51935
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                                                                                                                              Matches
                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                               overexpression of TGFbeta family proteins, including ectopic bone formation, psoriasis, muscular atrophy, scar formation, fibrosis cirrhosis. The present sequence is the human GDF8 protein.
                                                                                                                                                                                                                                                                                                     The present invention relates to muteins of a chain of a protein which, when in the form of a homodimer, has antagonistic or partial agonistic activity, and where the mutation results in the protein binding with low affinity to its receptor. The protein is a member of the transforming growth factor beta (TGFbeta) superfamily. The mutant sequences of the invention can be used in the treatment of diseases associated with the
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mutein of transforming growth factor-beta superfamily protein, useful for treating or preventing e.g. ectopic bone formation, competes for receptor binding -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; TGFbeta; transforming growth factor beta; mutant; antagonist; agonist; ectopic bone formation; psoriasis; muscular atrophy; scar; formation; fibrosis; cirrhosis; osteopathic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 6; 54pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-042559/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sebald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SEBA/) SEBALD W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000; 2000DE-1026713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antifibrotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TGFbeta protein superfamily protein GDF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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PKVSASHL----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                        DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY
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                                                                                                                            92;
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                                                                                                                                                 Similarity
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                                                                                                                                                                                                             109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nickel J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
                                                                                                                            Conservative
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                                                                                                                            1;
                                                                                                                       Score 501; DB 23;
Pred. No. 6.2e-47;
1; Mismatches 11;
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                                                                                                                                                                Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 109;
                                                                                                                          Indels
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                                                                                                                                                                                                                                                                       fibrosis and
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RESULT 6
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Best Local
          Growth differentiation factor-8; GDF-8; mouse; transctransforming growth factor-beta; muscle; meat; inhib; neuromuscular disease; muscular dystrophy; cachexia;
                                                                                                                07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDF-8 can be used to maintain cells before transplantation; to improve efficiency of cell fusion and to treat obesity or diseases related to abnormal adipocyte proliferation.
therapy.
                                                                               Murine growth
                                                                                                                                                   AAW69883;
                                                                                                                                                                                  AAW69883 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New growth differentiation factor 8 - use diagnosis of cell proliferative disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYJO ) UNIV JOHNS HOPKINS SCHOOL
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                                                                                                                                                                                                                                                              PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcpherron AC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 501; DB 15; Pred. No. 7.3e-47;
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                                                                               factor-8 C-terminal fragment.
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growth factor-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treatment ders esp. of muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                        transgenic animal; inhibitor; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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               AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                  126;
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                                                                                                                                                                                                                                    CC growth differentiation factor-8 (GDF-8), a novel member of the Cterminal portion of mouse CC growth differentiation factor-8 (GDF-8), a novel member of the Ctransforming growth factor-beta superfamily that appears to relate CC transforming growth factor-beta superfamily that appears to relate CC muscle, nerve and adipose tissue. The sequence was deduced from a CC partial genomic clone (see ANV45809). A full-length sequence (see CC ANW30689) has been deduced from a cDNA clone (see ANV42113). The CC GDF-8 expression is disrupted or interfered with. Also claimed are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb CC GDF-8 expression is disrupted or interfered with. Also claimed are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb CC animals by administering an antibody (Ab) that binds to GDF-8; (3) CC animals by administering an antibody (Ab) that binds to GDF-8; (3) CC animals by administering an antibody (Ab) that binds to GDF-8; (3) CC and encoding a GDF-8 protein truncated by loss of the C-terminal CC active fragment. The transgenic animals have increased muscle mass cc and for poultry reduced cholesterol contents. Method (3) is used to treat muscle wasting or neuromuscular diseases, muscular atrophy CC and capteve tissue and bone, or obstructive lung disease, AIDS can be used to maintain myobhasts intended for transplanting or to CC improve efficiency of fusion. Ab can be used to detect and CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring), CC also for immuncherapy and in vivo imaging.
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09833887-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-1997;
05-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus ap.
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 58; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-437444/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuromuscular disease
73 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 126
                    61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                           Local
                                                                                                        1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                     DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McPherron AC;
                                                                                                                                                           Similarity
                                                                                                                                                                                                                126 AA;
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0862445.
97US-0795071.
97US-0847910.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
13..14
16..17
17..126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "mature polypeptide"
                                                                                                                                                         80.4%;
                                                                                                                                        1; Mismatches
                                                                                                                                                         Score 501; DB 19;
Pred. No. 7.3e-47;
                                                                                                                                                                         Length 126;
                                                                                                                                          Indels
                                                                                                                                          10;
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1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60

Indels 10;

Gaps

2

Matches

Conservative

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RESULT 8
AAY15386
                                                                                                              Query Match
Best Local :
                                                                                                                                                                                      as ribs) when expressed in reduced amounts. GDF-8 minus transgenic animals and forms of animal feed that can inhibit/reduce production of GDF-8 are of commercial interest.

GDF-8 are of commercial interest.

GDF-8 expression may also have a role in the therapy of abnormal growth of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8 antisense molecule or dominant negative polypeptide could be used with foetal or adult muscle cells, bone cells or progenitor cells. These agents can be administered to a patient disorder muscle atrophy as muscle wasting disease, neuro muscular disorder, muscle atrophy as consequenced in the consequence of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the amino acid sequence of the C-terminal region of the GDF-8 precursor protein. The predicted GDF-8 sequence contains two potential proteolytic processing sites.

Cleavage of the precursor at the second of these sites would generate a mature C terminal fragment 109 amino acids in length with a predicted molecular weight of 12,400.

GDF-8 has been shown to result in increased bone and muscle mass (such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth differentiation factor; tissue growth; muscle growth; cell differentiation; animal feed; muscle disorder; bone degeneration; nerve degeneration; GDF-8; development; transforming growth factor beta; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-1998;
05-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-terminal region of mouse Growth Differentiation Factor-8 (GDF-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY15386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY15386 standard; Protein; 126 AA.
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 2a; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTSEGSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New differentiation factor useful for treating neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-494289/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage-site
                                                                                                                                                                  cell disorders, and aging for example.
                             Similarity
                                                                                                              126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0019070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US02511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Potential_proteolytic_cleavage_site
/note= "cleavage generates mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Potential_proteolytic_cleavage_site
                      80.4%;
Score 501; DB 20;
Pred. No. 7.3e-47;
1; Mismatches 11;
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                                       В
                                                                    Qy
                                                                                                                             Query Match
Best Local
                                                                                                           Matches
                                                                                                                                                                                                                            The present invention relates to growth differentiation factor-8 (GDF-8) cooling sequences and proteins. The present sequence is a GDF-8 protein, which was isolated in the present invention. GDF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200112777-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexi neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-211209/21.
N-PSDB; AAF63547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-2000; 2000WO-US22884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ds sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     traumatic injury; congestive obstructive pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine GDF-8 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB73182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB73182 standard; Protein; 126 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 2; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-2001
                                                                                                                                                                                                                    (COPD), AIDS or cachexia.
                                     73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                        1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McPherron AC;
                                                                                                                             Similarity
                                                                                                                                                                                   126 AA;
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0378238.
                                                                                                                           80.4%;
                                                                                                                           Score 501; DB 22; Pred. No. 7.3e-47;
                                                                                                           Mismatches
                                                                                                                                            Length 126;
                                                                                                           Indels
                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cachexia;
                                                                                                           Gaps
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AAB73189
  В
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                               The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a GDF-8 protein, which was isolated in the present invention. GDF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord treating muscle wasting disease, neuromuscular disorder, spinal cord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene therapy; growth differentiation factor-8; GDF-9; AIDS; cachexia; neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculdegenerative disease; tissue repair; muscule wasting disease; neuromuscular disorder; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB73189;
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Fig 2; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and cachexia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAF63555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-2000; 2000WO-US22884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 traumatic injury; congestive obstructive pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat GDF-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB73189 standard; Protein; 130
                                                                                                                                                                                                                                                                 (COPD), AIDS or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 126
  77
                                    61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                      Local
                                                                                                              1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
PHTHLVHQANPRGSAGPCCTPTKMSPINMLYENGKEQIIYGKIPAMVVDRCGCS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-211209/21.
                                                                           DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McPherron AC
                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                  traumatic injury, congestive obstructive pulmonary disease
                                                                                                                                                                                                                              130 AA;
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9905-0378238
                                                                                                                                                                  80.4%;
                                                                                                                                                                    Score 501; DB 22;
Pred. No. 7.5e-47;
                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                     Length 130;
                                                                                                                                                     10;
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RESULT 11.
AAB20153
                                                                                                 The present sequence is that of AutoVac construct GDF-8 ext, which consists of the C-terminal 160 amino acids of human growth differentiation factor 8 (GDF-8, see AAF20131) with residues 16-36 substituted by the promiscuous tetanus toxin T-cell epitope P30 (see AAB20144) and residues 37-51 substituted by tetanus toxin T-cell epitope P2 (see AAB20143). It is an object of the invention to produce a recombinant therapeutic vaccine that is capable of effecting down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth and of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation of GDF-8 in order to increase the muscle growth down-regulation order to increase
            of breaking autotolerance against autologous GDF-8. They comprise the C-terminal portion of human GDF-8 in which a portion of the native sequence is replaced by a T-cell epitope such as P30, with minimal disturbance of the authentic 3-dimensional structure of the protein. Nucleic acids encoding the GDF-8 variants can be used for genetic immunisation of the animals. Down-regulation of GDF-8 activity can increase muscle mass by up to at least 45% in cattle,
                                                                                                                                                                                                                                                                                                                                                                                                               regulating animal thro
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEBI-) M & E BIOTECH AS
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26-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB20153 standard;
                                                                                                                                                                                                                                                                                                                                                                                                      through induction of anti-GDF-8 antibody production
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                                                                                                                                                                                                                                                                                                                                                                                                                       the muscle mass of animals used in meat production by growth differentiation factor 8 (GDF-8) activity in t
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for meat production,
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Best Local s
                               The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a GDF-8 protein, which was isolated in the present invention. GDP-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord interval.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New substantially purified growth differentiation factor-8 pouseful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                Example 9; Fig 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexineurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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.5e-47;
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                                                                                                                                                                                                                                                                                                                             The present sequence is that of turkey growth differentiation factor 8 (GDF-8), also called myostatin. It is an object of the invention to produce a recombinant therapeutic vaccine capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. Variants of GDF-8 (see AAB20145-53) are provided that are capable of breaking autotolerance against autologous GDF-8. These comprise a C-terminal portion of human GDF-8 in which a portion of the native sequence is replaced by a T-cell epitope such as the promiscuous tetanus toxin T-cell epitope P2 or P30. Nucleic acids encoding the GDF-8 variants can be used for genetic immunisation of the animals. Down-regulation of GDF-8 activity is used to increase muscle mass by up to at least 45% activity is used to increase muscle mass by up to at least 45%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Turkey growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB20132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB20132 standard; Protein;
                                                                                                                                                                                                                      in cattle, pigs and poultry used for meat production, reducing the need for antibiotic feed-additives. Anti-GDF8 vaccines can be used to treat human diseases such as cancer cachexia where muscle atroph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2001
                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 76-78; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            animal through induction of anti-GDF-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MEBI-) M & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-2000; 2000WO-DK00413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulating
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                                                                                                                                                                                      pronounced and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the muscle mass of animals used in meat production by do growth differentiation factor 8 (GDF-8) activity in the growth differentiation of anti-DRF-8 anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOTECH AS
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99US-0145275
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                                                                                                                                                                                          patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klysner
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                                                                                                                                                                                          suffering
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cardiant; turkey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 1.4e-46;
smatches 11;
501;
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                                                                                                                                                                                              from acute
   DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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Query Match

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DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60

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RESULT 14
AAU75623
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                    Query Match
Best Local
                                                                                                                                                                                        factor (GDF) receptor, specifically a myostatin receptor, or its functional peptide portion. Also described is a method of modulating an effect of myostatin on a cell by contacting the cell with an agent that affects myostatin signal transduction in the cell. The method and the receptor are useful for ameliorating the severity of a pathological condition characterised by an abnormal amount, development or metabolic activity of muscle or adipose tissue in a subject, particularly a wastin disorder (e.g. cachexia, anorexia, muscular dystrophy or neuromuscular disease) or a metabolic disorder (e.g. obesity or type II diabetes). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective; antidiabetic; growth differentiation factor receptor; myostatin receptor; GDF; muscle tissue; adipose tissue; cachexia; wasting disorder; anorexia; muscular dystrophy; neuromuscular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for ameliorating wasting disdystrophy or neuromuscular disease obesity or type II diabetes .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New growth differentiation factor (GDF) receptors and modulators, useful for ameliorating wasting disorders such as cachexia, muscu dystrophy or neuromuscular disease or a metabolic disorder such a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLYU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUL-2000; 2000US-0626896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolic disorder; obesity; type II diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chicken promyostatin
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                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 22; Fig 1; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABK15396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee
                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a substantially purified growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309
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                                                                                                                                                 promyostatin.
                                                                                                                                                                         present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                       Similarity
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                                                                                                374 AA;
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                       80.4%;
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                                                                                                                                                                           order (e.g. obesity or type II diabetes). the amino acid sequence of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.4e
1; Mismatches
Score 501; DB 23;
Pred. No. 2.5e-46;
1; Mismatches 11;
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ches 11;
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                                                    Length 374;
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RESULT 15
AAR63160
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Search completed: March 25, 2003, 15:11:20 Job time: 73 secs
                                                                                                                                                   Matches
                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                        GDF-8 can be used to maintain cells before transplantation; to improve efficiency of cell fusion and to treat obesity or diseases related to abnormal adipocyte proliferation.
                                                                                                                                                                                                                                                                                                                                        WPI; 1994-316943/39.
Q-PSDB; Q76372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth differentiation factor-8; GDF-8; cell proliferation; adipocyte; obesity; transforming growth factor-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR63160 standard; Protein; 375 AA.
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                            Claim 3; Page 58; 84pp; English.
                                                                                                                                                                                                                                                                                                    New growth differentiation factor \theta - useful for treatment and diagnosis of cell proliferative disorders esp. of muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9421681-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human growth differentiation factor-8 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR63160;
                                                                                                                                                                                                                                                                                                                                                                            Lee S, Mcpherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                    (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                266 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY 320
                                                                                                                                                   92; Conservative
                                                                                                                                                                                                   375 AA;
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                                                                                                                                                80.4%; score 501; DB 15; Length 375;
80.7%; Pred. No. 2.5e-46;
ative 1; Mismatches 11; Indels 10; Gaps
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                           SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human: *
5: sp_mammal:*
5: sp_mammal:*
7: sp_mhc:*
8: sp_organelle
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_vrius:*
13: sp_vertebre
14: sp_unclassi
15: sp_vrius:*
16: sp_bacteria:*
16: sp_acteria::
17: sp_archeap:
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623
1 DFGLDCDEHSTESDCC
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
sp_fungi:*
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                                                                                                                                                                                                                                                           sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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SUMMARIES

16 46	15 46	14 46	13 46	12 46	11 48	10 48	9 49	8 49	7 49	6 50	5 50	4 50	3 50	2 50	1 501	Result No. Score
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373	373	373	385	389	185	185	375	375	375	375	375	375	375	375	162	ength
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	Q90zd2 oncorhynch	Q9ddi8 salmo sala:	Q90w05 sparus aura	Q90yy0 ictalurus p	Q9mz18 ovis aries	Q95nll capra hircu	Q8wns6 bos taurus	Q8uwe0 anas platyı		Q98sp0 gallus gal	Q8uwd7 coturnix cl	Q8uwd8 columba li	Q95j86 macaca fasc	Q9gm97 equus cabal	Q9tsy2 sus scrofa	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
214.5		214.5	214.5	215.5	215.5	215.5	217.5	217.5	221	225.5	230	253.5	253.5	255	257	262	286	293	415	426	447	456	458	462	463	463	463	463
34.4	34.4	34.4	4.			•			35.5	•			40.7	40.9	41.3	•	45.9	47.0	66.6		•		73.5	74.2		74.3		74.3
424	367	119	115	426	115	115	393	392	395	349	370	598	598	263	104	191	58	78	107	96	359	373	377	373	376	376	376	376
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Q98sp9 meleagris g	xenopus	Q95kpl ailurus ful	Q9dge9 cyprinus ca	omo sapi	Q9dge6 oryzias lat	Q9dgfl cyprinus ca	Q90261 brachydanio	Q9pwr8 carassius a		097138 brugia mala	\sim		Q9xz62 drosophila	umbrina ci	Q90z79 ictalurus p	4 pe		Q9xs86 equus cabal	Ø	Q9w759 cairina mos					umbrina	Q90wc8 morone amer		Q98tb4 oreochromis

ALIGNMENTS

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Match Local les 9	NON_TER SEQUENCE 16	ITE;	T; s		Pfam; PF00019; Pfam; PF00688;	InterPro;	InterPro;	; P1	AJ	SIMI	tati	omic	til	NE=	ENCE		MCBI_TaxID=9823;	ryot	Sus scrofa		tati	01-JUN-2002	01-MAY-2000	AY-2	Υ2;	¥2	
simi 2;	tein 1	PS0	M002	PR00	PF00019;	TP IF		8075	2379	LARI	n (G	org	Α.,	2007	FRO		ID=9	ه : ح			n (F	002					
80. Similarity 80. 2; Conservative	162 AA;	PROSITE; PS00250; TGF_BETA_1;	ProDom; PD000357; TGFb; SMART; SM00204; TGFB; 1.			IPROOIS39; TGFb	IPR002400; GF_cysknot	HSSP; P18075; 1BMP.	EMBL; AJ237920; CAB40844.1;	-!- SIMILARITY: BELONGS TO THE	myostatin (GDF8; MSTN) gene.";	"Genomic organization, sequence	Stratil A., Kopecny M.;	8370	SEQUENCE FROM N.A.		=9823;	Eukaryota; Metazoa;	(Pig).		Myostatin (Fragment).	(TrEMBLrel.	(TrE	(TrEMBLrel.		PREL	
ty erva		; TG	TGFB	GFC	GF-b	111;	400;	ΜP.	CAB4	BELO	MST	atio	cny	, Pu	Α.				•		ent)	MBLr	(TrEMBLrel.	MBLr		PRELIMINARY;	
80.4%; 80.7%; Live	1 18290 MW;	F_BE	Fb; 1.	YSKN	TGF-beta; 1. TGFb propeptide:	TGFb.	GF.		0844	NGS :	30 g	n, se	3	bMed:			Cera	Chor			•					ARY;	
% ;;) MW;	[A_1;	:	T.	1. optic	N.	cyskr		1: :	TO TH	ene.	equer		=106]			LLTTO	iata;				21, 1					
Score Pred.		٠.			le: 1		ot.		·		٠.٠	Ф		MEDLINE=20078370; PubMed=10612246;			cetartiodactyia; suina; suidae;	Chordata; Craniata; Vertebrata;				Last annotation update)	Last sequence update)	Created		PRT:	
e 501; . No. ismatc	3535									F-BE		and p					Ta;	miat				anno	sequ	ed)			
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Best Local
                                                                                                                                                                                                                                                                                                                                     InterPro; IPRO02048; EF-hand.
InterPro; IPRO01839; TGFb.
InterPro; IPRO01111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
                                                                                Q95J86;
Q95J86;
Q1-DEC-2001
01-DEC-2001
01-JUN-2002
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01-MAR-2001
01-MAR-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning of equine myostatin cDNA an myostatin in horse.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY EMBL; AB033541; BAB16046.1; -.
                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9796;
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           NCBI_TaxID=9541; [1]
                                 Cercopithecinae;
                                                                       Myostatin.
                                                                                                                                                                                                                                                                                                            Glycoprotein
                                                                                                                                                                                                                                                                                                                   PROSITE; PS00018; EF_HAND; UNKNOWN_1
PROSITE; PS00250; TGF_BETA_1; 1.
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  SEQUENCE FROM N.A
                                                             Macaca fascicularis
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                                                                                                                                                                           PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                           l Similarity
92; Conserv
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l (TrEMBLrel. 16,
2 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                375 AA; 42736 MW;
                                                                                 (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                           Conservative
                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Horse).
azoa; Chordata; Crania
eria; Perissodactyla;
                                 Macaca.
                                          Primates;
                                                 (Crab eating macaque) (Cynomolgus monkey). Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                   80.4%;
                                                                                Created)
Last sequence update)
Last annotation update)
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1; Mismatches
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e myostatin
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Last annotation update)
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ctyla; Equidae;
                                         Craniata; Vo
Catarrhini;
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                                       Cercopithecidae;
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                                                                                                                                                                  Query Match
Best Local S
Matches 92
                                                                                                                                                                                                                                           A Gu Z., Yang W., Cheng Z., Li H., Zhu D.;

"Molecular Cloning and Tissue Distribution of the

"Molecular Cloning and Tissue Distribution of the

Duck, Goose, Pigeon and Quail.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ da

EMBL; AF440863; AAJ35277.1; -

InterPro; IPR001839; TGFb_N.

R InterPro; IPR001839; TGFb_N.

R InterPro; IPR001111; TGFb_N.

Pfam; PF00019; TGF-beta; 1.

R Pfam; PF00688; TGFb_Dropeptide; 1.

R Pfam; PF00688; TGFb; 1.

R ProDom; PD000357; TGFb; 1.

R PROSITE; PS00018; EF_HAND; UNKNOWN_1.

R PROSITE; PS00018; EF_BETA_1; UNKNOWN_1.

SEQUENCE 375 AA; 42739 MW; 88296F0AE779476E
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Best Local S
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Q8UWD8;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
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Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein
SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
ProDom; PD000357; TGFb; 1.
PROSITE; PS00018: EF_HAND; UNKNO
PROSITE; PS00250; TGF_BETA_1; UNKNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Columba livia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=GASTROCNEMIUS;
                                                                               267
  322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322
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                                         61
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                                                                                                                           Н
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                                                                             HTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                           PKVSASHL - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKYSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                     Similarity
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                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Domestic pigeon).
cazoa; Chordata; Craniata; Vertebrata; Eutelo
ves; Neognathae; Columbiformes; Columbidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGF_BETA_1; UNKNOWN_1.
                                      -EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.4%;
                                                                                                                                                                                   80.4%;
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20,
21,
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                                                                                                                                                                  Score 501; DE Pred. No. 2e-5
1; Mismatches
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Pred. No. 2
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                                                                                                                                                                                                                                               88296F0AE779476E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence up
annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375
                                                                                                                                                                                     2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2e-52;
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                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                databases
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                                                                                                                                                                                                      Length
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bidae; Columba
                                                                                                                                                                                                             375;
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RESULT 5
Q8UWD7
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO02048; EF-hand.
InterPro; IPRO01839; TGFb.
InterPro; IPRO01111; TGFbb.
InterPro; IPRO01111; TGFbb.N.
Pfam; PF00688; TGFb-beta; I.
Probom; PF00688; TGFb-propeptide; 1.
Probom; PF000357; TGFb; I.
SMART; SM00204; TGFB; I.
SMART; SM00204; TGFB; I.
PROSITE; PS00250; TGF-BETA_1; UNKNOWN_1.
PROSITE; PS00250; TGF-BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Gu Z., Yang W., Cheng Z., Li H., Zhu D.,
Gu Z., Yang W., Cheng Z., Li H., Zhu D.,
Molecular Cloning and Tissue Distribution of the Myostatin Gene
Duck, Goose, Pigeon and Quail.",
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF440864; AAL35578.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coturnix chinensis.
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauría; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8UWD7;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Eukaryota: Aves: Neognathae: Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8UWD7
                                                                 EMBL; AF346599; AAK18000.1; HSSP; P18075; 1BMP.
                                                                                                   development.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                            Myostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q98SP0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0988P0
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InterPro; IPR001111; TGFb_N.
                                                                                                                                                                              Zhang Y., Yang W., Zhu D.;
"Genomic structure and expression of the chicken GDF-8 during
                    InterPro; IPR002048; EF-hand.
InterPro; IPR001839; TGFb.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92;
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80.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Indels 10;
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                                                                                                             RESULT 8
Q8UWE0
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pfam: pP00688; TGFb_propeptide; 1.
probom; pD000357; TGFb; 1.
SMARP; SM00204; TGFB; 1.
PROSITE; PS00018; EE; HAND; UNKNOWN_1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                           OHWE0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myostatin.
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                                                                                                                                                                                                                                                                                                                                                                                                            Local
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1 Similarity 80.7%;
92; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                           PRELIMINARY;
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RA GU Z. Fang W., Cheng Z., Li H., Zhu D.;

"Molecular Cloning and Tissue Distribution of the Myostatin Gene in Molecular Cloning and Tissue Distribution of the Myostatin Gene in Puck, Geose, Pigeon and Ouail.";

RI Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

RI InterPro; IPR002048; EF-hand.

RAIJ5276.1;

RI InterPro; IPR00189; TGFb.

RI InterPro; IPR00189; TGF-beta; I.

R Pfam; PF00019; TGF-beta; I.

R Pfam; PF00688; TGFb-bcta; I.

R Pfam; PF00688; TGFb-bcta; I.

R PFAm; PF005157; TGFb; I.

R PROSITE; PS00204; TGFB; 1.

R PROSITE; PS002018; EF-HAND; UNKNOWN 1.

R PROSITE; PS002018; EF-HAND; UNKNOWN 1.

R PROSITE; PS002018; EF-HAND; UNKNOWN 1.
OBUWED;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein,
SEQUENCE 375 AA; 42717 MW; D980E286426E4D4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anser anser (domestic goose).
Eukaryota; Metazoa; Chordatta; Craniata; Vertebrata; Euteleostomi;
Archosauria; Ayes; Neognathae; Anseriformes; Anatidae; Anser.
                                                                                                                                                                                                                                       322 PHTHLVHQANPRGPAGPCCTPTKMSPINMLYENGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                              267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF----VFLQKY 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.5%; Score 495; DB 13; Length 375; 79.8%; Pred. No. 1.1e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
   Last sequence update)
Last annotation update)
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Pred. No. 2.6e-52;
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels i 10; Gaps
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RY Molecular Cloning and Tissue Distribution of the Myostatin Gene in RY Duck, Goose, Pigeon and Ouail. ";

RY Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

REMBL, RAF40861, AAL5375.1; -.

RINterPro; IPRO01839; TGFb.

RINterPro; IPRO01839; TGFb.N.

RINterPro; IPRO01819; TGFb.N.

PR InterPro; IPRO01819; TGFb.N.

R Ffam; PF000688; TGFb_Dropeptide; 1.

R Pfam; PF000687; TGFb_STGFb; 1.

R PFAM; PF000687; TGFb; 1.

R PROSTIE; PS00018; EF-HAND; UNKNOWN 1.

SR SEQUENCE 375 AA; 42817 MW; 1BA7FF5225C23620 CRC64;
                                                                                                                       Query Match
Best Local
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Best Local :
                                                                                            Matches · 90;
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Bos taurus (Bovine).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                         Pfam; PF00019; TGF-beta; T.

Pfam; PF00688; TGFb_propeptide; 1.

ProDom; PF000357; TGFb; 1.

SMART; SM00204; TGFB; 1.

SRART; SM00204; TGFB; 1.

SROSITE; PS000218; EF-HAND, UNKNOWN_1.

PROSITE; PS000250; TGF_BERAL; UNKNOWN_1.

SEQUENCE 375 AA; 42524 MW; 0EC27616C202F5E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002048; EF-hand.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shibata M., Muramoto T., Aikawa K.;
"Genomic organization and sequence of the myostatin gene in bovine.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB076403; BAB79498.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08WNS6
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Ayes; Neognathae; Anseriformes; Anatidae; Anas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSEECEF----VFLQKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
1 DFGLDCDEHSTESRCCRYPLTVDFBAFGWDWIIAPKRYKANYCSGECEENNETVSFWLRV 60
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1 Similarity 79.8%;
91; Conservation
                                                                                                                          Similarity
                                                                                            Conservative
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                                                                                                                78.7%;
78.9%;
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Last annotation updat
                                                                                        pred. No. 4.30
2; Mismatches

    Mismatches

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                                                                                            12; indels 10;
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Q95N11
ID Q95N1
AC Q95N1
DT Q95N1
DT Q95N1
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DT 01-DE
CAPT
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9MZ18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lian Z., Pan Q., Chen H., Jin H., Li N.;
"Cloning of intron 2 of the myostatin gene in goat.";
submitted (APR 2001) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AY032689; AAK49790.1;
InterPro; IPR001189; TGFb.
InterPro; IPR001111; TGFb.N.
"Cloning of intron 2 of the myostatin gene in sheep."; "Cloning of intron 2 of the myostatin gene in sheep."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. EMBL; AF266758; AAF78069.1; -.
                                                                                                                                                                                                     Mammalia; Eutheria; Cetz
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                             Ovis aries (Sheep).
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Mammalia; Eutheria; Cetar
Bovidae; Caprinae; Capra.
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                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                      Myostatin (Fragment).
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01-JUN-2002
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                                                                                                                                                  SEQUENCE FROM N.A.
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PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
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Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 QKYPHTHLVHQANPKGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPGMVVDRCG 185
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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20953 MW;
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78.3%;
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Last annotation update)
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16; Gaps

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RESULT
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AC QS
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Best Local S
Matches 89
                                                                                                                                                                                                               "Molecular Characterization and expression of the myo channel catfish (Ictalurus punctatus).";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databas
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AF396747; AAK84666.1; -.
EMBL; AF396747; AAK84666.1; -.
InterPro; IPR001131; TGFb.N.
InterPro; IPR001111; TGFb.N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb-bropeptide; 1.
PF00575; PGF000357; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
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                                                                                                                                                                Query Match
Best Local :
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Q90YYO,
01-DEC-2001 (TREMBLEGL. 1
01-DEC-2001 (TREMBLEGL. 1
01-JUN-2002 (TREMBLEGL. 2
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InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_Propeptide; 1
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
 Q90W05
Q90W05;
                                                                                                                                                                                                                                                                                                                                                                              Ictalurus punctatus (Channel catfish).
Eukaryota; Metazoa; Chordata; Craniata;
Acthopterygii, neopterygii; Teleostei;
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                   Ictaluridae; Ict
NCBI_TaxID=7998;
                                                                                                                                                                                                                                                                                                                                                                                                                          Myostatin.
                                                                                                                                                                                                           Glycoprotein
                                                                                                                                                                                                                                                                                                                                      Kocabas A.M., Liu Z.J.;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                               GLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRVPK 62
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                                                                                       VSASHL-----
                                                                                                         GLDCDENSSESRCCRYPLTVDFEDFGWDWIIAPKRYKANYCSGECDY-----VHLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P12643;
                                                                                                                                                      84;
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                                                                                                                                                               Similarity
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185
185 AA;
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            PRELIMINARY;
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
20923 MW;
                                                                                      EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                              43600 MW;
                                                                                                                                                               74.6%;
73.0%;
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77.48;
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19,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 480;
Pred. No. 3.
                                                                                                                                                  Pred. No. 4./6
3; Mismatches
                                                                                                                                                              Score 465; DB 13; Length Pred. No. 4.7e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BA9634203A552850 CRC64;
                                                                                                                                                                                              569FB952B7E9E173 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389
            385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; I
3.2e-50;
hes 8;
                                                                                                                                                                                                                                                                                                                                                                                           Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
            A
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                                                                                                                                                                                                                                                                                                       databases
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                                                                                                                                                                                                                                                                                                                          myostatin
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                                                                                                                                                                                                                                                                                                                                                                                           Siluriformes;
                                                                                                                                                                          389;
                                                                                                                                                     16;
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                                                                  389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 85
                                                                                                                                      Ostbye T.K., Galloway T.F., Nielse "The two myostatin genes of Atlant expressed in a variety of tissues."
                                                                                                                                                                                                                                                                       Q9DD18;
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2001 (TrEMBLrel. 18,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of the myostatin gene in the gilthead: Sparus aurata: sequence, genomic structure, and expressic submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. -!-SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. EMBL; AF258448; AAK53545.1; -. EMBL; AF258447; AAK53544.1; -.
                                                                                                                                                                                                        Salmo salar (Atlantic salmon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Verta Actinopterygii; Neopterygii; Teleostei; Eute Acanthomorpha; Acanthopterygii; Percomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
"The two myostatin genes of Atlantic expressed in a variety of tissues."; Submitted (AUG-2001) to the EMBL/GenE
                                            Ostbye T.K.,
                                                                                                                                                                                                                                                                                                                       8Iddeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein
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NCBI_TaxID=8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sparus aurata (Gilthead sea bream)
                                   Andersen O.;
                                                         SEQUENCE FROM N.
                                                                                 Submitted
                                                                                             Andersen
                                                                                                       SEQUENCE
                                                                                                                              Submitted
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=8030;
                                                                                                                                                                                                                                                                 Myostatin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patarnello T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maccatrozzo L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                 329
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85; Conserv
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                                                                                                      FROM
                                                                                (AUG-2001)
                                                                                                                             (DEC-2000)
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                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                               Galloway
                                                                                                      N.A.
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                                                                                                                             to the
                                              T.F.,
                                                                                                                                                  T.F., Nielsen (
                                                                                 the
   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
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                                                Nielsen
                                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 464; DB 13;
Pred. No. 6.2e-48;
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Radaelli G.,
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lmon (Salmo
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Euteleostei; Neoteleostei;
rpha; Perciformes; Percoide
                                               Gabestad I., Bardal T.,
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                        (Salmo
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                        salar)
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RESULT
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Best Local S
Matches 85
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Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                       Glycoprotein.
Glycoprotein.
GROUPENCE 373 AA; 42049 MW;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
Pr0D0m; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PR0SITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. EMBL; AF273035; AAK71707.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rescan P.-Y., Jutel I., Ralliere C.;
"Two myostatin genes are differentially expressed of the trout (Oncorhynchus mykiss).";
J. Exp. Biol. 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myostatin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q90ZD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Signal.
SIGNAL 22 F
CHAIN 265 373 N
SEQUENCE 373 AA; 41896 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. EMBL; AJ297267; CAC19541.2; -. EMBL; AJ316006; CAC59700.1; -. HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8022;
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InterPro; IPR001111; TGFb_N.
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317 QKYPHTHLVNKANPRGTAGPCCTPTKMSPINMLYFNRKEQIIYGKIPSMVVDRCGCS 373
                                                     61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
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                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                     1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                          DSGLDCDENSPESRCCRYPLTVDFEDFGWDWIIAPKRYKANYCSGECEY------MHL
                                                                                                                                                                                                                    85;
                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.3%;
72.6%;
                                                                                                                                                                                                                                       74.3%;
                                                                                                                                                                                                              Score 463; DB 13;
Pred. No. 7.9e-48;
6; Mismatches 10;
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Last sequence update)
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Pred. No. 7.9e-48;
6; Mismatches 10;
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MYOSTATIN.
, C641D71D83E66C4D CRC64;
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                                                                                                                                                                                                                                                                                                                           9DD4771B5CF671EA CRC64;
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                                                                                                                                                                                                                                                                   Length 373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myotomal muscle
                                                                                                                                                                                                                 16;
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                                                                                                                                                                                                              Gaps
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                                                                                                          316
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Search completed: March 25, 2003, 15:12:19

Job time : 35 secs

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Title:
Perfect
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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BMP6_MOUSE
IHBA_CHICK
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                                                                               SEQUENCE
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ALIGNMENTS	DVR1_BRARE GDF6_MOUSE GDF6_BOVIN GDF7_MOUSE BMP2_RAT BMP2_MOUSE BMP2_MOUSE BMP2_DAWDA BMP2_CHICK BMP2_CHICK BMP2_XENLA BMPB_XENLA
	p35621 brachydanio p43028 mus musculu p55106 bos taurus p43029 mus musculu p49001 rattus norv p21274 mus musculu 04554 oryctolagus 019006 dama dama (p12643 homo sapien 090751 gallus gall p25703 xenopus lae p30884 xenopus lae

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restrained by the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Double muscling in cattle due to mutations in the myostatin proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=White leghorn; TISSUE=Skeletal muscle; MEDLINE=98024153; PubMed=9356471;
                                                                                                                                                                                                                                                                                                                                                                                        pfam; pri00019; TGF-beta; 1.
pfam; pr00688; TGFb_propeptide;
proDom; pD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                         ProDom; PDUUU35/; 1988;
SMART; SM00204; TGFB;
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InterPro; IPR001111; TGFb_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                          AA;
                                                                                                                                                                                                                                                                                                                  Cytokine;
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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     80.4%;
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POTENTIAL.
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  Score 501; DB 1;
Pred. No. 3.1e-48;
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N-LINKED (GLCNAC. . .) (POT
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GROWTH/DIFFERENTIATION FACTOR
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ID GDF8.H
AC 014793
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RC MADLIN
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PROSITE; FU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE SYVOLLINE SYVOLUT SYVOLU
    DISULFID
                                                                                                                                                                                                Pfam; PF00019; TGF-beta; 1. Pfam; PF00688; TGFb_propeptide; Pr0Dom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McPherron A.C., Lee S.-J.;

McPherron A.C., Lee S.-J.;

"Double muscling in cattle due to mutations in the myostatin gene.";

"Double muscling in cattle due to mutations in the myostatin gene.";

"Double muscling in cattle due to mutations in the myostatin gene.";
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDF8 OK Noin.
Homo sapiens (Human).
Morazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99061972; PubMed=9843994;
Gonzalez-Cadavid N.F., Taylor W.E., Yarasheski K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Skeletal muscle;
MEDLINE=98024153; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                  DISULFID
                                                                                               PROPEF
                                                                                                                                                                                  SMART; SM00204; TGFB;
                                                                                                                                                                                                                                                                     InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMODIMER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUSCLE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                            601788; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY
                                                                                                                                                                                                                                                                                                                                                                     P18075;
                                                                                                                                                                                                                                                                                                                                                                                          AF019627; AAB86694.1; AF104922; AAC96327.1;
                                                                                                                                                                                                                                                                                                                                           HGNC:4223; GDF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92;
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                                                                                                                                                                                                                                                                                                                                                                     1BMP
                                                                                                                                     Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                               TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=9356471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE-LINKED (BY SIMILARITY)
                                                                                                               Glycoprotein; Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
       84
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84
                                                           POTENTIAL.
GROWTH/DIFFERENTIATION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
  Y SIMILARITY.
Y SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene and expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ki K., Sinha-Hikim
Mamita M., Nair G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321
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GDF8_MI
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CARBOHYD
SEQUENCE
                                                                                                                                                        DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MELGA
                                                                                          SEQUENCE
                                                                                                                  CARBOHYD
                                                                                                                                       DISULFID
                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001839;
InterPro; IPR001111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                          SIGNAI
                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                             SMART; SM00204;
                                                                                                                                                                                                                                                                                                                                                                  ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDF8_MELGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUSCLE GROWTH
  92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity 80.
92; Conservative
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                     PD000357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375
                                                                                            375
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aves;
                                                                                                                                                                                                                                                                        Cytokine;
1 23
                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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                                                                                                                                                                                                                                                                                                                                           TGFB;
                                                                                                                                                                                                                                                                                                                                                                  TGFb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339
71
42750
                                                                                                                                     266
375
340
372
374
339
                                                                                          42784
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042221;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Double muscling in cattle due to mutations in the myostatin gene."; Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Crania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth/differentiation factor 8 precursor (GDF-8) (Myostatin)
                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF019625; AAB86692.1; HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98024153; PubMed=9356471;
McPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SI SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
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                                                                                                                                                                                                                                                                                                                 PS00250; TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Meleagrididae; Meleag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.4%;
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80.7%;
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                                                                                                                                                                                                                                                                  Glycoprotein;
POTENTIAL.
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1;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PO
; EBFF6129725E6AFA CRC64;
                     Pred. No. 3.1e-48
                                          Score 501;
                                                                                                                                                   GROWTH/DIFFERENTIATION FACTOR
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                           INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PC
                                                                                                                                                                                                                                               POTENTIAL.
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Mismatches
                                                                                      D2AEAB732AEB4E77 CRC64;
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                                                                                                                                                                                                                                                                                       Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions
                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1e-48;
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                                       Length 375
Indels
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Gaps
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                                                                                                                     EMBL; AF019623; AAB86690.1; EMBL; AF188635; AAF02770.1; EMBL; AF188635; AAF02771.1; EMBL; AF188638; AAF02772.1; EMBL; AF188638; AAF02773.1; EMBL; AF033855; AAC08035.1; EMBL; AF033955; AAC08035.1; EMBL; AF033793; AAC02489.1; HSSP; P18075; 1BMP.
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018831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDF8 OR MSTN
                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by
                                                                                                                                                                                                                                                                                                                                                                                             Daneau I., Silversides D.W.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ
-!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-98024153; PubMed-9356471;
McDherron A.C., Lee S.-J.;
"Double muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Voelker G.R., Conroy J.C., Wheeler M.B.;
"Porcine myostatin cDNA sequences: Duroc, Hampshire, Meishan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                              InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Muscl
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-10 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yorkshire pigs.";
Submitted (SEP-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                           Pfam; PF00688; TGFb_propeptide;
Probom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                   Pfam; PF00019;
Pfam; PF00688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMODIMER;
                                                                                                                                                                                                                                                                                                                                                                                   MUSCLE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNETVSFWLRV
               factor;
                                                                              8075; 1BMP.; IPR001839; TGFb.; IPR0018111; TGFb_N.; IPR001111; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hampshire, Meishan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
 Cytokine; Glycoprotein;
1 23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      36-375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                         TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                       DISULFIDE-LINKED
                                                                                                                                        ......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Yorkshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375
                 Signal
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                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                   databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                    OF,
                                                                                                                                                                                                                                                                                                                                                                                                     SKELETAL
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Best Local
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CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDF8_MOUSE
008689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _MOUSE
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CD-1; TISSUE-Skeletal muscle; MEDLINB=97884412; PubMed=9139826; McPherron A.C., Lawler A.M., Lee S.-J.; "Regulation of skeletal muscle mass in m superfamily member.";
                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth/differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   Nature 387:83-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDF8 OR MSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                  EMBL; U84005; AAC53167.1; HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322
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                                                                                                                                                                                                                                                               MUSCLE GROWTH.
SUBUNIT: HOMODIMER; DISULPIDE-LINKED (BY SIMILARITY).
SUBUNIT: HOMODIMER; DISULPIDE-LINKED (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND AD
SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.
SKELETAL MUSCLE: WEAK EXPRESSION IN ADIPOSE TISSUE.
DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-COLTUM IN
DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION
DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION
                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                       CONTINUES IN ADULTHOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
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267
281
309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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375
340
372
374
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339
71
72791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor 8 precursor (GDF-8) (Myostatin).
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GROWTH/DIFFERENTIATION FACTOR 8
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 501; DB 1; Pred. No. 3.1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0F658685EFDA3418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                              TGF-beta
                                                                                                                                                                                           restrictions on
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                                                                                                                                                                     and
                                                                                                                                                                                                          EMBL
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                                                                                                                                                                                                                   collaboration
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                                                                                                                                                                                                         outstation
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MGD; MGL; PUOVA, IRRO01839; TGFb_N. InterPro; IPR001811; TGFb_N. Pfam; PF00019; TGF-beta; 1. Pfam; PF00688; TGFb_propeptide; PF00688; TGFb_TFFb; 1.

MGD; MGI:95691;

Gdf8

ProDom; PD000357; TGE SMART; SM00204; TGFB;

PS00250;

TGF_BETA_1;

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RESULT 6
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Best Local
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DISULFID
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SIGNAL
PROPEP
DISULFID
                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, I
16-OCT-2001 (Rel. 40, I
Growth/differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDF8_RAT ST/
035312;
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                         DISULFID
                                                                                                       ProDom; PD000357; TGF
SMART; SM00204; TGFB;
                                                                                                                             InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                        "Double muscling in cattle due to mutations in the myostatin gene.", Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
              DISULFID
                                        CHAIN
                                                                  SIGNAL
                                                                             Growth factor;
                                                                                                                                                                                     EMBL; AF019624; AAE86691.1; HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDF8 OR MSTN
                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                    McPherron A.C., Lee S.-J
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98024153; PubMed=9356471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: ACTS SPECIFICALLY AS
                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                               MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                            PS00250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 AA;
                        268
282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                Cytokine; Glycoprotein; Signal.

1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                          muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                    TGFb;
                                                                                            TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
n factor 8 precursor (GDF-8) (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 501; Db 1,
No. 3.1e-48;
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Ув
Ув
                       GROWTH/DIFFERENTIATION FACTOR 8. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PO
                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GROWTH/DIFFERENTIATION FACTOR 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3E19814DD62C08BE CRC64;
SIMILARITY
              SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                             A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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STITE TO THE TENT OF THE TENT 
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GDF8_SHEEP
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                 HSSP, PIBU/J, IRGEB.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   018830;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
                                                                        CARBOHYD
CARBOHYD
                                                                                                                                              DISULFID DISULFID
                                                                                                                                                                                               CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98024153; PubMed=9356471;
McPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
,
,CBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDF8
                                                 SEQUENCE
                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                             Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF019622; AAB86689.1; HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Double muscling in cattle due to mutations in the myostatin gene."; Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF-----VFLQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUSCLE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR MSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKVSASHL----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                       SM00204; TGFB; 1.
SM00204; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                             Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340
72
42829
                                                                             266
375
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374
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71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.4%;
     80.3%;
                                                                                                                                                                                                                                                                                             Glycoprotein; Signal.
                                                   WW,
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                                                                      INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PO
N-LINKED (GLCNAC. . .) (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 501;
Pred. No. 3
     Score 500;
                                                                                                                                            GROWTH/DIFFERENTIATION FACTOR
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PO
; 933043D8C8C3294B CRC64;
                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                   1C36F3833BB11241 CRC64;
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8.1e-48;
  DB
  1:
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Length 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                        (POTENTIAL)
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GDT8_PAPHA
ID GDT8_P

AC 01828
DT 15-UIL
DT 15-UIL
DT 15-UIL
DT 15-UIL
DT 16-OCT
DE GROWTH
GN GDF8 0
OC Mammall
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                                                              Matches
                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                       ProDom; Puvovou
SMART; SM00204; TGFB; 1.
SMART; SM002050; TGF_BETA_1;
PROSITE; PS00250; TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8)
                                                                                                                                             DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDF8 OR MSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             018828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDF8_PAPHA
                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                          InterPro; IPR001111; TGFb_N.
pfam; pF000019; TGF-beta; 1.
pfam: PF00688; TGFb_propeptide;
proDom; pD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF019619; AAB86686.1; HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced the between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Double muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-I- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98024153; PubMed=9356471; McPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Papio hamadryas (Hamadryas baboon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                             PROPEP
                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
   267
                                H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER; SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEF--
Similarity
                                                                               Similarity
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                                                                                                                               375
                                                                                                                                                  24
267
281
309
313
339
                                                                Conservative
                                                                                                                               AA;
                                                                                                                                                                                                                                                                          Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscle;
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                                                                                                                                                  266
375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.6%;
                                                                                                                               42688 MW;
                                                                              79.5%;
79.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFIDE-LINKED (BY SIMILARITY).
TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2,
                                                                                                                                                                           POTENTIAL.
GROWTH/DIFFERENTIATION F
GROWTH/DIFFERENTIATION F
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                              Pred. No. 1.4e
1; Mismatches
                                                                       Score 495; UB 1,
                                                                                                                                             INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                            7B49B90ACAB926EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and the
                                                                                               Length 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                FACTOR
                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restrictions
      -----VFLQKY 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outstation
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                                                                  Gaps
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S
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      RESULT
GDF8_B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kambadur R., Sharma M., Smith T.P. "Mutations in myostatin (GDF8) in Piedmontese cattle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Friesian; TISSUE=Muscle, a MEDLINE=97458167; PubMed=9314496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDF8_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21343337; PubMed=11451380; Jeanplong F., Sharma M., Somers W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANTS STRAIN-Holstein; TISSUE-Skeletal MEDLINE-98024153; PubMed=9356471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 7:910-916(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                      EMBL;
HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene.
                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: ACTS SPECIFICALLY AS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322
                                                                                                    or send an email to license@isb-sib.ch).
                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUSCLE GROWTH.
                         AF320998;
P18075; 1
                                                                     AF019761;
                                                    AF019620;
          IPR001839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                    AAB81508.1;
AAB86687.1;
                                   AAB86687.1;
AAG48116.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND VARIANT MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220:31-37(2001)
          TGFb
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O18836; O18829; Q95N97;
15-JUL-1998 (Rel. 36, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Growth/differentiation factor 8 precursor (GD GDF8 OR MSTN OR MH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Boyidae; Boyinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING AND SKELETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIMB MUSCLES M.SEMIMEMRANOSUS AND M.BICEPS FEMORIS; LOW LEVELS IN OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Double muscling in cattle due to mutations in the myostatin gene."; Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jeanplong F., Sharma M., Somers W.G., Bass J.J., "Genomic organization and neonatal expression of
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                 - DEVELOPMENTAL STAGE: WIDELY EXPRESSED THROUGHOUT DEVELOPMENT.

LOW LEVELS ARE FOUND UP TO DAY 29 EMBRYOS. LEVELS INCREASE FROM
DAY 31 UP UNTIL LATE GESTATION.

DISEASE: DEFECTS IN GDF8 ARE THE CAUSE OF THE DOUBLE-MUSCLE
PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIVE
DISEASE FREQUENTLY FOUND IN THE BELGIAN BLUE AND PIEDMOTESE
CATTLE BREEDS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED
NUMBER OF MUSCLE FIBERS (HYPERPLASIA), RESULTING IN AN INCREASE
MUSCLE MASS OF 20-25%.

STATILBETTAGE TO THE STATE OF T
                                                                                        European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor (GDF-8)
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nd Embryo;
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DE GROWTH
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Best Local :
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Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-98024153; PubMed-9356471;
MCPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDF8 OR MSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDF8_BRARE
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                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      "Double muscling in cattle due to mutations in the myostatin gene.", Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
       InterPro; "IPR001111; TGFb_N
                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio)
                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                    MUSCLE GROWTH.
                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS
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                                                   ZDB-GENE-990415-165; gdf8
                                                                               P18075;
                                                                                                    AF019626; AAB86693.1;
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                              IPR001839;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGFD;
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78.9%;
                              TGFb
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N-LINKED (GLCNAC. . . ) (
F -> L (IN MH; PIEDMONTE
C -> Y (IN MH; PIEDMONTE
C -> T (IN REF. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 490;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> L (IN MH; PIEDMONTESE BREED).
-> Y (IN MH; PIEDMONTESE BREED).
-> T (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84E1AB20650C05F6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDFB_MOUSE STANDARD; PRT; 405 AA. 9921M4; 090x55; 09R221; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) 17-OCT-2001 (Rel. 40, Last annotation update) 18-OCT-2001 (Rel. 40, Last annotation update) 19-OCT-2001 (Rel. 40, Last 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                              McPherron A.C., Lawler A.M., Lee S.-J.; "Regulation of anterior/posterior patterning of the axial skeleton growth/differentiation factor 11.";
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129/SvJ;
MEDLINE=99318097; PubMed=10391213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=99177155; PubMed=10075854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1;
                                                                                                                                  BMP/TGFbeta superfamily during mouse embryogenesis. Mech. Dev. 80:185-189(1999).
                                                                                                                                                                                           MEDLINE=99173787; PubMed=10072786; Nakashima M., Toyono T., Akamine A., J
"Expression of growth/differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dev. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bud is a potent mesoderm inducer in Xenopus embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gamer L.W., Wolfman N.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDF11 OR BMP11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                          SEQUENCE OF 75-405 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A novel BMP expressed in developing mouse limb,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 QKYPHTHLVNKASPRGTAGPCCTPTKMSPINMLYFNGKEQIIYGKIPSMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 DSGLDCDENSSESRCCRYPLTVDFEDFGWDWIIAPKRYKANYCSGECDY-------MYL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                    TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN. SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY)
                                                                                             FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
SUBCELLULAR LOCATION:
                                                                      PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                                                                                                                                                                                                                                           Genet.
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72.6%;
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POTENTIAL.
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Secreted (Probable)
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (POTENTIAL).
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Pred. No. 1.4e-44;
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Sciurognathi;
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                                                                                                                                                                                              Joyner A.;
n factor 11,
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thi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 374;
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SOLITIFIED TO SERVICE OF SERVICE 
                                                                                                                                    RESULT 12
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CONFLICT
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InterPro; IPR001111; TGFb_N.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
PF0000357; TGFb; 1.
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                              GDFB_HUMAN
095390; Q9U
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EMBL;
HSSP;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1338027;
              Growth/differentiation
                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                    349 QKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVVDRCGCS
                                                                                                                                                                                                                                                                                                   297
                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED DOMAINS AT 8.5 DAYS POST COITUS (DPC) WHERE IT IS HIGHEST IN THE TAIL BUD. AT 10.5 DPC, EXPRESSED IN THE BRANCHTAL ARCHES, LIMB BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED IN TERMINALLY-DIFFERENTIATED ODONTOBLASTS, THE NASAL EPITHELIUM, RETINA AND SPECIFIC REGIONS OF THE BRAIN.

SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD, 'INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZIN TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADUDENTAL PULP AND BRAIN.
                                                                                                                                                                                                                                                                                                                      DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV: ||||||||:||: : :
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P18075; le
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AF028335;
AF028336;
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                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                              Q9UID1; Q9UID2;
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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AAF21633.1;
AAD05267.1;
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                                                                                                                   STANDARD;
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213
270
402
404
404
171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44946
                                                                                                                                                                                                                                           -EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                        75.0%;
71.8%;
                 factor 11 precursor (Bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
BY SIMILARITY.
GROWTH/DIFFERENTIATION FACTOR 11.
POLY-ALA.
POLY-GLY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
E -> G (IN REF. 3).
T -> N (IN REF. 2).
MW; A74E382710A14781 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOINED
                                                                                                                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED
                                                                                                                                                                                                                                                                                                                                                                                                        Score 467; DB 1
Pred. No. 2e-44;
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                       407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                     A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 405;
                   morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                299
                       61
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                   InterPro; IPRUULLUJ,
InterPro; IPR001111; TGFb_N.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
                                                                                                                                                    DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                   CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF100907; AAC72852.1;
EMBL; AF028333; AAF21630.1;
EMBL; AF028334; AAF21631.1;
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth/differentiation factor 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bud is a potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen V.; "A novel BMP expressed in developing mouse limb, spinal cord, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fetal brain; MEDLINE=99177155; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDF11 OR BMP11
                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McPherron A.C., Lawler A.M., Lee 9
"Regulation of anterior/posterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99318097;
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                         Growth factor;
                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                  SMART; SM00204;
                                                                                                                                                                                                                                                                                                                                                                                                           Genew;
                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genet. 22:260-264(1999).

Genet. 22:260-264(1999).

FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANYENIGK/POSTERIOR AXIS DURING DEVELOPMENT.

PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.

SUBUNIT: HOMODIMER: DISULFIDE-LIXKED (BY SIMILARITY).

SUBCELLULAR LOCATION: Secreted (Probable).

SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
                                                                                                                                                                                                                                                                                                                                                                                               603936;
PKVSASHL---
                                                   DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV
: |||||||:||:
                                      NLGLDCDEHSSESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGQCEY------MFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L.W., Wolfman
                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:4216; GDF11.
                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                    PS00250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208:222-232(1999).
                                                                                                                                                                    299
210
210
313
341
345
371
                                                                                          Conservative
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                                                                                                                                                                                                                                                                                         Cytokine;
                                                                                                                                                                                                                                                                                                                TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mesoderm inducer in Xenopus embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10391213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10075854;
an N.M., Celeste
                                                                                                                                                                                                                                                                                                    TGF_BETA_1;
                                                                                                                                                         24
298
407
41
215
215
215
372
404
404
406
371
                                                                                                    75.0%;
71.8%;
                                                                                                                                            45090
            -EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                         Glycoprotein; Signal.
                                                                                                                                            MW;
                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . . ) (POT)
                                                                                         8;
                                                                                                      Score 467; DB 1
Pred. No. 2e-44;
                                                                                                                                                                                                                                                             POTENTIAL.
BY SIMILARITY
                                                                                                                                                                                                                        POLY-GLY
                                                                                                                                                                                                                                   POLY-ALA
                                                                                                                                                                                                                                                  GROWTH/DIFFERENTIATION FACTOR
                                                                                                                                           E8FF48E363635BA8 CRC64;
                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  А.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patterning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the
                                                                                          9;
                                                                                                                  Length 407;
                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 axial skeleton
                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hewick
                                                                                          16;
                                                                                         Gaps
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351 QKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVVDRCGCS 407

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GRESULT 13
GREENLY 13

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Best Local
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"Expression of growth/differentiation factor 11, a new member of the BME/TGEbeta superfamily during mouse embryogenesis.";

Mech. Dev. 80:185-189(1999).

1 FONCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL TIDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.

1 IDENTITY ALONG THE ANTERING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN (BY SIMILARITY).

1 SUBURIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

1 SUBURIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 11 precursor (Bone morphogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9Z217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDFB_RAT
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99173787; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDF11 OR BMP11.
                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00019; TGF-beta; 1
Pfam, PF00688; TGFb_propeptide;
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF092733; AAD05266.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                      Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                           243
              295 QKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVV 345
                                                     61
                                                                                                                              1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFNNFTVSFWLRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                         NLGLDCDEHSSESRCCRYPLTVDFEASGWDWIIAPKRYKANYCSGQCEY-----
                                  PKVSASHL-----EAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00204; TGFB;
                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00250;
                                                                                                                                                                                                                                            38
345
345 AA;
                                                                                                                                                                                                                                                                                                        154
257
315
                                                                                                                                                                                                                                                                                                                                                           243
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Δ
                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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>345
159
316
315
- 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=10072786;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TGF_BETA_1; 1
                                                                                                                                                                                                                                                 39094 MW;
                                                                                                                                                                                     67.48;
                                                                                                                                                                     8
                                                                                                                                                                                     Score 420; DB 1;
Pred. No. 2.7e-39;
                                                                                                                                                                                                                                                                                   INTERCHAIN
N-LINKED (G
                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                               GROWTH/DIFFERENTIATION FACTOR 11.
                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
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                                                                                                                                                                                                                                               81D5B93FED6B0443 CRC64;
                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345
                                                                                                                                                                                                                                                                               (GLCNAC. . .) (PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
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                                                                                                                                                                                                        Length 345;
                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                   (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                     103
                                                                                                                                                                     16;
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                                                                                           MFM 294
                                                                                                                                                                     Gaps
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IHBB_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Albano P.M., Groome N., Smith J.C.;

"Activins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their differentiation.";

Development 117:711-723(1993).

-i. FUNCTION: INHIBITS AND ACTIVINS INHIBIT AND ACTIVATE,

-i. FUNCTION: THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Activin disrupts epithelial branching morphogenesis in developing glandular organs of the mouse."; Mech. Dev. 50:229-245(1995).
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-234 FROM N.A. STRAIN=CBA X NMR1; TISSUE=Testis; MEDLINE=95344997; PubMed=7619733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).
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Q1-FEB-1994 (R6
                                                                                                                                                                                   MGD; MGI:96571; Inhbb.
                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                               PIR; S31441; S31441.
                                                                                                                                                                                                                                                                           EMBL; X83376; CAA58290.1;
EMBL; X69620; CAA49326.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ritvos O., Tuuri T., Eramaa M., Sainio K., Hilden K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-A.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
TISSUE SPECIFICITY: UTERUS, TESTIS, OVARY, LUNG,
CJ7 EMBRYONIC STEM CELLS, AND POSSIBLY IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVINS.
SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS
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ng as its content
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Growth factor; Hormone; Glycoprotein.
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POTENTIAL

INHIBIN BETA B CHAIN

Prodom; PD000357; TGFE; SMART; SM00204; TGFE;

PROSITE;

PS00250; TGF_BETA_1; 1.

CHAIN

a collaboration

outstation

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 311-381 FROM N.A.
MEDLINB-91029482; PubMed=2225063;
MITTARN E., Ziv T., Thomsen G., Shimc
"Activin can induce the formation of
in the hypoblast of the chick.";
Cell 63:495-501(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-White leghorn; TISSUE-Ovary;
Hecht D.J., Davis A.J., Ryan I.M., Johnson P.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Follicle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A MUMBER OF DIVERSE
FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
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EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                             ACTIVINS.
SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-A.
ACTIVIN B IS A HOMODIMER OF BETA-B.
ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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Pred. No. '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
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Pfam; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
PRODOm; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1
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Growth factor;
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IAB235 IAB235 IAB235 IAB235 IAB236 N;Alternate names: activin bB chain C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 01-Aug-1997 #text. C;Accession: IAB235; IAB286; S31441 R;Ritvos, 0.; Tuuri, T.; Eramaa, M.; Sainio, K.; Hilden, Mech. Dev. 50, 229-245, 1995 A;Title: Activin disrupts epithelial branching morphogen A;Reference number: IAB235; MUID:95344997; PMID:7619733 A;Accession: IAB235 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-234 <ress 117,="" 1993<="" 711-723,="" a;cross-references:="" development="" embl:x83376;="" groome,="" j.c.="" n.;="" nid:9603571;="" pidn:caa58="" r.m.;="" r;albano,="" smith,="" th=""><th>Query Match 36.9%; Score 230; DB 2; Length 370; Best Local Similarity 37.48; Pred. No. '2.7e-17; Matches 46; Conservative 17; Mismatches 36; Indels 24; G Qy 3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DMILAPKRYKANYCSGECEENNFTVSFMLRVP </th><th>RESULT 1 151199 activin beta B subunit - African clawed frog C; Species: Xenopus laevis (African clawed frog) C; Species: Xenopus laevis (African clawed frog) C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text C; Accession: 151199 R; Dohrmann, C.E.; Hemmati-Brivanlou, A.; Thomsen, G.H.; Dev. Biol: 157, 474-483, 1993 A; Title: Expression of activin mRNA during early develop A; Reference number: 151199; MUID:93273083; PMID:8500654 A; Accession: 151199 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-370 CODH> A; Residues: 1-370 CODH> A; Cross-references: GB:S61773; NID:g386027; PIDN:AAB2686 C; Superfamily: inhibin</th><th>30 203 32.6 396 1 BMHU2 31 202 32.4 398 2 JH0688 32 202 32.4 398 2 JH0688 33 202.5 32.4 398 2 JH0687 34 201.5 32.3 31.4 25 149542 35 197.5 31.7 452 1 HMHU5 36 197.5 31.7 454 1 BMHU5 37 197.5 31.7 451 2 S42408 39 195.5 31.4 316 2 S42408 40 195.5 31.4 313 2 I51184 40 195.5 31.4 313 2 I51184 41 195.5 31.4 316 2 A25619 42 195.5 31.4 316 2 A25619 43 194.5 31.2 495 2 A45056 44 194.5 31.2 495 2 S43294</th></ress>	Query Match 36.9%; Score 230; DB 2; Length 370; Best Local Similarity 37.48; Pred. No. '2.7e-17; Matches 46; Conservative 17; Mismatches 36; Indels 24; G Qy 3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DMILAPKRYKANYCSGECEENNFTVSFMLRVP	RESULT 1 151199 activin beta B subunit - African clawed frog C; Species: Xenopus laevis (African clawed frog) C; Species: Xenopus laevis (African clawed frog) C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text C; Accession: 151199 R; Dohrmann, C.E.; Hemmati-Brivanlou, A.; Thomsen, G.H.; Dev. Biol: 157, 474-483, 1993 A; Title: Expression of activin mRNA during early develop A; Reference number: 151199; MUID:93273083; PMID:8500654 A; Accession: 151199 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-370 CODH> A; Residues: 1-370 CODH> A; Cross-references: GB:S61773; NID:g386027; PIDN:AAB2686 C; Superfamily: inhibin	30 203 32.6 396 1 BMHU2 31 202 32.4 398 2 JH0688 32 202 32.4 398 2 JH0688 33 202.5 32.4 398 2 JH0687 34 201.5 32.3 31.4 25 149542 35 197.5 31.7 452 1 HMHU5 36 197.5 31.7 454 1 BMHU5 37 197.5 31.7 451 2 S42408 39 195.5 31.4 316 2 S42408 40 195.5 31.4 313 2 I51184 40 195.5 31.4 313 2 I51184 41 195.5 31.4 316 2 A25619 42 195.5 31.4 316 2 A25619 43 194.5 31.2 495 2 A45056 44 194.5 31.2 495 2 S43294
t_change 16-Jul-1999 , K.; Saxen, L.; Gilbert, S.F. nesis in developing glandular 8290.1; PID:g603572	ngth 370; Indels 24; Gaps 4; CEFUNETVSFWLRVP 61 :: CPAYLAGVP 307 QIIYGKIPAMVVDRC 106 : : : NIVKRDVPNMIVDEC 367	<pre>ext_change 16-Jul-1999 1.; Fields, A.; Woolf, T.M.; Melt plopment in Xenopus laevis. 554 26863.1; PID:g386028</pre>	bone morphogenetic bone morphogenetic bone morphogenetic bone morphogenetic bone morphogenetic activin beta-A cha bone morphogenetic bone morphogenetic bone morphogenetic consequence of the control of

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R; Feng, Z.M.; Li, Y.P.; Chen, C.L.C.

NJ. Endocrinol. 3, 1914-1925, 1989

A;Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit gelence number: A41398; MUID:90190649; PMID:2628729

A; Accession: B41398
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                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Complementary deoxyribonucleic acid (cDNA) cloning A;Reference number: A40905; MUID:90331931; PMID:2484214 A;Accession: C40905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Two messenger ribonucleic acids encoding the common A;Reference number: I53288; MUID:94307180; PMID:8033818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M32756; GB:M32757; NID:g204943; PIDN:AAA41438.1; PID:g554460 R;Dykema, J.C.; Mayo, K.E. Endocrinology 135, 702-711, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: inhibin/activin beta B-chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Apr-1992 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C;Accession: B41398; I53288; C40905
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 134,'D',136-255 <ALB>
A;Cross_references: EMBL:X69620; NID:g50147; PIDN:CAA49326.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Esch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:S72477; NID:g619268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-7 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: I53288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-174 <FEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sh, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno, Endocrinol. 1, 385-396, 1987
                              349 GSASSFHTAVVNQYRMRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDVPNMIVEEC
                                                                                                                                        297
                                                                                     62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 GLECDGRT--SLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCP-----AYLAGVP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 GCA 255
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                                                                                                                                                                         3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFNNFTVSFWLRVP 61
                                                                                                                                                                                                                                                            Joca 1
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                                                                                                                           GLECDGRT--SLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCP-----AYLAGVP 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -KVSASH-----LEAGP----CCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRC 106
                                                                                                                                                                                                                                     48;
                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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39.0%;
                                                                                                                                                                                                                                                       36.6%;
                                                                              --LEAGP----CCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRC 106
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                                                                                                                                                                                                                                   16;
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                                                                                                                                                                                                                              Score 228; DB
Pred. No. 5e-1
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 228; DB 2;
Pred. No. 3.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibin beta-B chain precursor - human
N;Alternate names: activin AB chain B
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000
C;Accession: A40150; C;24248; A40156; S;0751
                                               R; Feng, Z.M.; Bardin, C.W.; Chen, Mol. Endocrinol. 3, 939-948, 1989
                                                                                                                                                                                                                    A;Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; R;Mason, A.J.; Niall, H.D.; Seeburg, P.H. Biochem. Biophys. Res. Commun. 135, 957-964, 1986
A;Title: Structure of two human ovarian inhibins.
                    A; Title: Characterization and regulation of testicular inhibin beta-subunit mRNA
                                                                      A;Cross-references: GB:M13437; NID:g186416; PIDN:AAA59169.1; PID:g186417 R;Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.
                                                                                                                                                                                                                                                                                                                                                                                        R;Mason, A.J.; Berkemeier, L.M.; Schmelzer, C.H.; Schwall, R.H. Mol. Endocrinol. 3, 1352-1358, 1989
A;Title: Activin B: precursor sequences, genomic structure and A;Reference number: A40150; MUID:90114200; PMID:2575216
                                                                                                                      A; Molecule type: mRNA
A; Residues: 55-407 < MA2>
                                                                                                                                                                      A;Reference number: A90123; MUID:86186863; PMID:3754442
A;Accession: C24248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:X03267; NID:g2005; PIDN:CAA27021.1; PID:g2006
C;Comment: The source of this protein is ovarian follicular fluid.
C;Comment: The mature protein is the carboxyl-terminal segment of a precursor polypep ifferent forms of inhibin have been isolated (A and B) that differ in the amino-termi C;Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of fol
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C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Jun.1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                         A;Residues: 1-407 <MAS>
                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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A; Residues: 1-349 < MA
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MUID:89295443;
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PMID:2739657
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precurs

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A;Cross-references: GDB:119347; OMIM:147390
A;Map position: 2cen-2q13
C;Superfamily: inhibin
C;Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
F;1-20/Domain: signal sequence #status predicted <810>
F;21-292/Domain: propeptide #status predicted <PRO>
F;293/Product: inhibin beta-B chain #status predicted <MAT>
F;93/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A40156
A;Molecule type: mRNA
A;Residues: 22-46, 'A', 48-407 <FEN>
A;Cross references: GB:M3132
A;Experimental source: testis
R;Schmelzer, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Ma
Biochim. Biophys. Acta 1039, 135-141, 1990
A;Title: Purification and characterization of recombinant human
A;Reference number: $10751; MUID:90304183; PMID:2364091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 293-294, 'GX', 297-302, 'XX', 305-307
C; Comment: Activins A and B are homodimers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                         $50899

betaB inhibin precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change

C;Accession: $50899
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                   R;Thompson, D.A.; Cronin, C.N.; Martin, F.
Eur. J. Biochem. 226, 751-764, 1994
A;Title: Genomic cloning and sequence analyses of the bovine y DNase I footprinting.
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A;Accession: S50899
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C; Superfam
                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: U16240
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A; Residues: 1-408 <TH
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                                                                                                                                                               Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEENNFTVSFWLRVP
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KVSASHLEA--
                                                                      GLECDGRT--NLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCP-----AYLAGVP 345
                                                                                                         GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFNNFTVSFWLRVP 61
                                                                                                                                                                                                                                           151/1
                                                                                                                                                44;
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44; Conservative
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                                                                                                                                                Conservative
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35.8%;
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                                                                                                                                              ; Score 218; DB 2; Pred. No. 6e-16; 18; Mismatches
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Pred. No.
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                                   -GPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRC 106
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                                                                                                                                                                                 2;
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                                                                                                                                                 37;
                                                                                                                                                                                 Length 408;
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R;Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E. Blochem. Blophys. Res. Commun. 193, 711-717, 1993
A;Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural A;Reference number: PN0504; MUID:93290666; PMID:8512569
A;Accession: PN0506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Carassius auratus (goldfish)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0506
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(;Species: Brachydanio rerio (zebra fish)
C;Date: 13:Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I50103
R;Wittbrodt, J.; Rosa, F.M.
Genes Dev. 8, 1448-1462, 1994
Gens Dev. 8, 1448-1462, 1994
A;Reference number: I50103; MUID:95011555; PMID:7926744
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A; Residues: 1-115 <GEW>
C; Superfamily: inhibin
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N;Alternate names: gact 11
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A;Molecule type: mRNA
A;Residues: 1-393 <WIT>
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Best Local :
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                                                                                                                                                                                      Local Similarity
                                                                                                                                 3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFNNFTVSFWLRVP
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       GCS 109
                                   GSASSFHTAVVNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEEC
                                                                      KVSASHLEA
                                                                                                     GLECDGNN-GGLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCP----
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pred. No. 1.9e-16;
5; Mismatches 39;
                                                                -GPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRC 106
                                                                                                                                                                      Score 217.5; DB 2
Pred. No. 6.6e-16;
8; Mismatches 38
                                                                                                                                                                                                     DB 2;
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                                                                                                          -AYMAGVP
                                                                                                                                                                                                                                                                                           PID:g516357
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391

GCA 393

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activin beta C precursor - mouse (Species: Mus musculus (house mouse) C:Species: Mus musculus (house mouse) C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change C:Accession: S70580 Matzuk, M.M. Matzuk, M.M. Biochim. Biophys. Acta 1307, 145-148, 1996 A:Title: Structural analysis of the mouse activin beta-C gene. A:Reference number: S70580; MUID:96283807; PMID:8679697
                                                                                                                                                        RESULT
S70580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: JC5366; R;Fang, J.; Wang, S.; Smiley, E.; Bonadio, J. Biochem. Biophys. Res. Commun. 231, 655-661, 1997 A;Title: Genes coding for mouse activin beta C and beta A;Reference number: JC5366; MUID:97224404; PMID:9070865 A;Accession: JC5366
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C;Comment: Activin beta C and
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A; Residues: 1-352 <FAN>
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A;Title: Cloning and sequencing of goldfish activin subunit genes: A;Reference number: PN0504; MUID:93290666; PMID:8512569
A;Accession: PN0505
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C;Species: Carassius auratus (goldfish)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0505
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A; Residues: 1-115 <GEW>
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                                                                                                                                                                                                                                                       57 WLRVPKVSASHLEA-----GPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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37.0%;
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                                                                                                                                                                                                                                                                                                                                                                        Score 216.5; DB 2
Pred. No. 7.5e-16;
7; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 216.5; DB 2
Pred. No. 2.4e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a distinct subset of related activins
                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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                                                                                           26-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                      Gaps
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C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision
C;Accession: A60087; I48265; S31440
                                                                       N; Alternate names: activin A; mesoderm-inducing
                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:X03266; NID:g2002; PIDN:CAA27020.1; PID:g2003 C;Comment: The source of this protein is ovarian follicular fluid. C;Comment: The mature protein is the carboxyl-terminal segment of a precursor polypep ifferent forms of inhibin have been isolated (A and B) that differ in the amino-termi C;Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of fol C;Superfamily: inhibin
                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;21-308/Domain: propeptide #status predicted <PRO>F;309-424/Product: inhibin beta-A chain #status predicted F;165/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: contraceptive; follitropin inhibitor; glycoprotein; gonad F;1-20/Domain: signal sequence #status predicted SIG>
                                                                                                  inhibin beta-A chain - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Complementary DNA sequences of ovarian follicular fluid inhibin show A;Reference number: A93371; MUID:86092207; PMID:2417121 A;Accession: A01393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibin beta-A chain precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C;Accession: A01393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-424 < MAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Mason, A.J.; Hayflick, Nature 318, 659-663, 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-352 <LAU>
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                                                                                                                                                                                                                                                                                                                       309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 HTAVLNLLKANAAAGTTGRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 GIDC--QGASRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASF 294
                                                                                                                                                                                                                                                            50 NNFTVSFWLRVPKVSASHLEAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                           GLECD--GKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSF 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WLRVPKVSASHLEA-----GPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                 34.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 215.5; DB 1;
Pred. No. 1.2e-15;
21; Mismatches 38;
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Pred. No. 7.5e-16;
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A;Title: A mesoderm-inducing factor produced by WEHI-3 murine A;Reference number: A60087; MUID:92155098; PMID:2133547 A;Accession: A60087

R;Albano, R.M.; Godsave, S.F.; Huylebroeck, Development 110, 435-443, 1990

D.;

Van Nimmen, K.; Isaacs, H.V.;

myelomonocytic leukemia

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A;Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis of A;Reference number: A40905; MUID:90331931; PMID:2484214
A;Accession: B40905
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-424 <ESCS
R;Woodruff, T.K.; Meunier, H.; Jones, P.B.C.; Hsueh, A.J.W.; Mayo, K.E.
Mol. Endocrinol. 1, 561-568, 1987
A;Title: Rat inhibin: molecular cloning of alpha- and beta-subunit complementary deoxyri
A;Reference number: A40056; MUID:91042598; PMID:3153478
A;Accession: B40056
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A; Cross-references: EMBL: X69619; NID: g50145; PIDN: CAA49325.1; C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 309-311, 'X', 313-318, 'XX', 321-325 <AL2>
R; Albano, R.M.; Groome, N.; Smith, J.C.

Development 117, 711-723, 1993
A; Title: Activins are expressed in preimplantation mouse A; Reference number: I48243; MUID:93321614; PMID:8330535
A; Accession: I48265
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
N;Alternate names: activin; mesoderm inducing factor C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: S50898; B25732; A60960; B61548 R;Thompson, D.A.; Cronin, C.N.; Martin, F. Eur. J. Biochem. 226, 751-764, 1994 A;Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A
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A;Residues: 1-366,'H',368-424 <WOO>
A;Cross_references: GB:M37482; NID:g204936; PIDN:AAA41436.1; PID:g204937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibin beta-A chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999  #sequence_revision 10-Sep-1999  #text_change 10-Sep-1999
C;Date: 10-Sep-1999  #sequence_revision 10-Sep-1999  #text_change 10-Sep-1999
C;Accession: B40955
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                                                                                                                                             inhibin beta-A chain precursor - bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
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                                                                                                                                                                                                                                                     SSTVINHYRMRGHSPFANLKS--CCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGCS
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Pred. No. 1.2
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Pred. No. 1.2e-15;
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  bovine alpha-, beta(A)-
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C;Superfamily: inhibin
C;Keywords: disulfide bond; glycoprotein; gonad; heterodimer; homodimer; hormone
F;1-28/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Forage, R.G.; Ring, J.M.; Brown, R.W.; McInerney, B.V.; Cobon, Proc. Natl. Acad. Sci. U.S.A. 83, 3091-3095, 1986
A;Title: Cloning and sequence analysis of cDNA species coding for A;Reference number: A94097; MUID:86205842; PMID:3458167
A;Accession: B25732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Iga
Mol. Cell. Endocrinol. 44, 55-60, 1986
A;Title: Isolation of bovine follicular fluid inhibin of
A;Reference number: A61548; MUID:86136989; PMID:3081385
A;Accession: B61548
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A; Status: preliminary
A; Molecule type: DNA
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A;Title: Mesoderm-inducing factor from bovine amniotic fluid:
A;Reference number: A60960; MUID:92126853; PMID:2133067
A;Accession: A60960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M13274; NID:g163196; PIDN:AAA97415.1; PID:g163197 A;Note: part of this sequence, including the amino end of the mature pro R;Chertov, O.Y.; Krasnosel'skii, A.L.; Bogdanov, M.E.; Hoperskaya, O.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 258-425 <FOR>
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A; Reference number:
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Reference number: S50897; MUID:95112839; PMID:7813465
                                                                                                                                                                                                                                           Matches
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completed:
ne : 43 secs
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                                                                                                                                                            310 GLECD--GKVNICCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSF
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                                                                            HSTVINHYRMRGHSPFANLKS--CCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEBCGCS
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                   March
                   25,
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36.7%;
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